

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 18:57:00 1997; MasPar time 1002.71 Seconds

Tabular output not generated.

Title: >US-08-699-716A-1
Description: (1-1566) from US08699716A.seq
Perfect Score: 1566
N.A. Sequence: 1 ATGGGCCATCATCATCATCA.....ATGACACGTCTGTTAATGA 1566
Comp: TACCCGGTAGTAGTAGTAGT.....TACTGGACAGACCATTTACT

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS

1:EST9 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99

Database:

EST-STS-TWO

100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129
130:EST130 131:EST131 132:EST132 133:EST133 134:EST134
135:EST135 136:EST136 137:EST137 138:EST138 139:EST139
140:EST140 141:EST141 142:EST142 143:EST143 144:EST144
145:EST145 146:EST146 147:EST147 148:EST148 149:EST149
150:EST150 151:EST151 152:EST152 153:EST153 154:EST154
155:EST155 156:EST156 157:EST157 158:EST158 159:EST159
160:EST160 161:EST161 162:EST162 163:EST163 164:EST164
165:EST165 166:EST166 167:EST167 168:EST168 169:EST169
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

BEST AVAILABLE COPY

Statistics: Mean 11.349; Variance 2.120; scale 5.354
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description	Pred. No.
	1	33	2.1	451	197	G09413	human STS CHLC.ATC1.P	3.12e-18
	2	32	2.0	231	81	M43926	yy45g10.r1 Homo sapie	1.07e-16
	3	31	2.0	239	197	G08851	human STS CHLC.ATC3C1	3.44e-15
	4	31	2.0	255	251	PCU64650	Parachartergus colobo	3.44e-15
	5	31	2.0	255	205	PCU64650	Parachartergus colobo	3.44e-15
	6	31	2.0	255	204	PCU64650	Parachartergus colobo	3.44e-15
	7	31	2.0	256	196	G08117	human STS CHLC.ATC3B0	3.44e-15
	8	31	2.0	298	203	HSB346BYB5	H.sapiens (D152781) D	3.44e-15
	9	32	2.0	314	197	G08591	human STS CHLC.ATC6.P	1.07e-16
	10	31	2.0	377	197	G09253	human STS CHLC.ATC2C0	3.44e-15
	11	31	2.0	514	19	ATTS1025	A. thaliana transcrib	3.44e-15
	12	32	2.0	521	205	H0WUT7996	Human STS UT7996.	1.07e-16
	13	32	2.0	521	204	H0WUT7996	Human STS UT7996.	1.07e-16
	14	31	2.0	588	197	G09471	human STS CHLC.ATC5A0	3.44e-15
	15	30	1.9	277	197	G09999	human STS CHLC.GC116B	1.04e-13
	16	30	1.9	311	197	G10330	human STS CHLC.ATC7F0	1.04e-13
	17	30	1.9	326	205	H0WUT8005B	Human STS UT8005, 3'	1.04e-13
	18	30	1.9	326	204	H0WUT8005B	Human STS UT8005, 3'	1.04e-13
	19	30	1.9	332	197	G09256	human STS CHLC.ATC3C1	1.04e-13
	20	30	1.9	334	197	G10329	human STS CHLC.ATC6F1	1.04e-13
	21	30	1.9	339	197	G09261	human STS CHLC.ATC2F0	1.04e-13
	22	30	1.9	342	204	H0WUT7997	human STS UT7997.	1.04e-13
	23	30	1.9	342	205	H0WUT7997	human STS UT7997.	1.04e-13
	24	30	1.9	345	197	G09257	human STS CHLC.ATC2B1	1.04e-13
	25	30	1.9	359	104	R23641	YH35e02.r1 Homo sapie	1.04e-13
	26	30	1.9	366	204	H0WUT1040	Human STS UT1040.	1.04e-13
	27	30	1.9	366	205	H0WUT1040	Human STS UT1040.	1.04e-13
	28	30	1.9	366	196	G08221	human STS CHLC.ATC3A0	1.04e-13
	29	30	1.9	372	85	HSPD03455	H.sapiens EST sequenc	1.04e-13
	30	30	1.9	372	222	HSPD03455	H.sapiens EST sequenc	1.04e-13
	31	30	1.9	395	197	G08663	human STS CHLC.ATC2D1	1.04e-13
	32	30	1.9	397	197	G09248	human STS CHLC.ATC2B1	1.04e-13
	33	30	1.9	403	197	G09249	human STS CHLC.ATC2C0	1.04e-13
	34	30	1.9	407	54	H85715	y568g06.r1 Homo sapie	1.04e-13
	35	30	1.9	416	92	M78296	EST00444 Homo sapie	1.04e-13
	36	30	1.9	444	204	H0WUT6615	Human STS UT6615.	1.04e-13
	37	30	1.9	444	205	H0WUT6615	Human STS UT6615.	1.04e-13
	38	30	1.9	521	140	R76963	Y166a07.r1 Homo sapie	1.04e-13
	39	29	1.9	554	55	H91490	SMNCA073SK Brugia ma	2.97e-12
	40	30	1.9	559	198	G15746	human STS CHLC.ATC5H0	1.04e-13
	41	30	1.9	588	197	G09469	human STS CHLC.ATC4C0	1.04e-13
	42	30	1.9	625	197	G09478	human STS CHLC.ATC4D0	1.04e-13
	43	30	1.9	634	205	H0WUT6629	Human STS UT6629.	1.04e-13

44	30	1.9	634	204	HUMUT6029	Human	STS	UT6629.	1.04e-13
45	30	1.9	661	197	G09464	human	STS	CHLC.ATCAAO	1.04e-13

ALIGNMENTS

RESULT	1			
LOCUS	G09413	451 bp	DNA	STS
DEFINITION	human STS	CHLC.ATC1.19551	clone ATC1.	
ACCESSION	G09413			
NID	6941262			
KEYWORDS	STS sequence; primer; sequence tagged site.			
SOURCE	human vector-pUCpl host-E.coli dut+ung+ (DH10B) Marker Selected			
	genomic DNA prepared from AT individual of French nationality.			
ORGANISM	Homo sapiens			

Primer A: CATCACCATTGTACCCATCA
Primer B: CCACCTGGTCTAGCAATGTT
STS size: 133
PCR profile:

denature:	30 seconds at 94 degrees C
annealing:	75 seconds at 55 degrees C
extension:	15 seconds at 72 degrees C
PCR cycles:	27
extension:	6 minutes at 72 degrees C

Template:	30ng genomic DNA
Primer:	each 1.5 pmole
dNTPs:	each 200 μ M
Tag Polymerase:	0.3 units
Total Vol:	10 μ l

MgCl ₂ :	1.5mM
KCl:	50mM
Tris:	10mM

FEATURES

Location/Qualifiers
1..451

STS

```

primer_bind      complement(262..301)
BASE COUNT      134 a      92 c      78 g      137 t      10 others
ORIGIN

```

Query Match	2.18;	Score 33;	DB 197;	Length 451;
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Db      245  catcatcatcatcatcatcatcatcaacaag 275/
      |||
QY      7  CATCATCATCATCATCATCATCATCAGCAG 41

```

RESULT 2

LOCUS	N43926	231 bp	mRNA	EST	07-FEB-1996
DEFINITION	yy45g10.r1 Homo sapiens CDNA clone 276546 5'				
ACCESSION	N43926				
NID	g1182454				
KEYWORDS	EST.				
SOURCE	human clone=276546 primer=T7 library=Scars multiple sclerosis				

ORGANISM

REFERENCE
AUTHORS
1 (pages 1 to 231)
Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Ratkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The Washo-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estewatson.wustl.edu
High quality sequence stops: 183
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers
1..231

```

/organism="Homo sapiens"
/clone="276546"
<1..>231
mRNA

```

65 a	43 c	41 g	80 t	2 others
------	------	------	------	----------

Query Match	2.0%;	Score 32;	DB 81;	length 231;
Best Local Similarity	90.0%;	Pred. No. 1.07e-16;		
Matches	36;	Conservative 0;	Mismatches 4;	Indels 0;
			Gaps	0

```

Db      137  gctatcatcatcatcatcatcatcatccctgcagtgg 176
        |||||||
QY      5   gccatcatcatcatcatcatcatcatcagcagcgg 44

```

RESULT	3
LOCUS	G08851 239 bp DNA STS
DEFINITION	human STS CHLC.ATC3C12.P7566 clone ATC3C12.
KEYWORDS	
REFERENCE	
DATE	08-AUG-1999

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrastoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

ACCESSION U64650
NID 91495941
KEYWORDS STS.
SOURCE Parachartergus colobopteranus.
ORGANISM Parachartergus colobopteranus.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Apocrita;
Aculeata; Vespoidea; Vespidae; Polistinae; Parachartergus.
REFERENCE 1 (bases 1 to 255)
AUTHORS Strassmann, J.E., Solis, C.R., Barefield, K. and Queller, D.C.
TITLE Trinucleotide microsatellite loci in a swarm-founding neotropical
wasp, Parachartergus colobopteranus and their usefulness in other
social wasps
JOURNAL Mol. Ecol. 5 (3), 459-461 (1996)
MEDLINE 96266704
REFERENCE 2 (bases 1 to 255)
AUTHORS Strassmann, J.E., Hughes, C.R., Barefield, K., Solis, C.R. and
Queller, D.C.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-1996) Ecology & Evolutionary Biology, Rice
University, 6100 Main, Houston, TX 77005, USA
FEATURES
source Location/Qualifiers
1..255
/organism="Parachartergus colobopteranus"
/clone="Paco3301CAT"
satellite 1..255
/note="microsatellite"
primer_bind complement(137..156)
repeat_region 164..208
primer_bind 236..255
BASE COUNT 59 a 57 c 90 g 49 t
ORIGIN
Query Match 2.0%; Score 31; DB 204; Length 255;
Best Local Similarity 100.0%; Pred. No. 3,44e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 179 tgtatgatgatgatgatgatgatgatg 209
|||||
Cp 37 TGTGATGATGATGATGATGATGATGATG 7
RESULT 7
LOCUS G08117 256 bp DNA STS 08-AUG-1995
DEFINITION human STS CHLC.ATC3E01.P7574 clone ATC3E01.
ACCESSION G08117
NID 9938667
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
ORGANISM Homo Sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Cathartini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: ATC3E01, CHLC.ATC3E01.#T7573
CONTACT: Dr. Jeffrey C. Murray
DOI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@iowa.edu
Primer A: GCTGGCATGATAAATGCTT
Primer B: AAATGGCCACTCCCTAAAC
STS size: 147
PCR Profile: denature: 30 seconds at 94 degrees C

annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 uL
Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3.
FEATURES
source Location/Qualifiers
1..256
/organism="Homo Sapiens"
STS 7..153
primer_bind 7..26
primer_bind complement(134..153)
BASE COUNT 58 a 37 c 62 g 80 t 19 others
ORIGIN
Query Match 2.0%; Score 31; DB 196; Length 256;
Best Local Similarity 100.0%; Pred. No. 3,44e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 78 tgaatgatgatgatgatgatgatgatg 108
|||||
Cp 35 TGATGATGATGATGATGATGATGATGATG 5
RESULT 8
LOCUS HSB346YB5 298 bp DNA STS 24-MAR-1996
DEFINITION H.sapiens (DIS2781) DNA segment containing (CA) repeat; clone
AFMB346YB5; single read.
ACCESSION 253778
NID 91235224
KEYWORDS CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA;
microsatellite marker; repeat polymorphism; STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Cathartini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 298)
AUTHORS Weissenbach, J.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
E-mail: Jean.Weissenbach@genethon.fr
REFERENCE 2 (bases 1 to 298)
AUTHORS Dib, C., Faure, S., Fizames, C., Samson, D., Drouot, N., Vignal, A.,
Millaudeau, P., Marc, S., Hazan, J., Seboun, E., Lathrop, M., Gyapay, G.,
Morissette, J., and Weissenbach, J.
TITLE A comprehensive genetic map of the human genome based on 5,264
microsatellites
JOURNAL Nature 380 (6570), 152-154 (1996)
MEDLINE 96176476
COMMENT full automatic.
FEATURES
source Location/Qualifiers
1..298
/organism="Homo sapiens"
/note="Cloning vector is M13mp18"
/cell_line="CEPH 134702"
/clone_id="genomic DNA"
/chromosome="1"
BASE COUNT 90 a 107 c 33 g 66 t 2 others
ORIGIN
Query Match 2.0%; Score 31; DB 203; Length 298;
Best Local Similarity 97.0%; Pred. No. 3,44e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	212	catcatcatcatcatcatcatcgtcatcagc	244
Oy	7	CATCATCATCATCATCATCATCATCATCATCAAC	39
RESULT	9		
LOCUS	G08591	314 bp	DNA
DEFINITION	human STS	CHLC.ATC6.P9593	clone ATC6.
ACCESSION	G08591		
NID	9939141		
KEYWORDS	STS sequence; primer; sequence tagged site.		
SOURCE	human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.		
ORGANISM	Homo Sapiens		
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates		
AUTHORS	Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 314)		
JOURNAL	Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H. Cooperative Human Linkage Center Unpublished (1995)		
COMMENT	Synonyms: ATC6, CHLC.ATC6. #T9592 Contact: Dr. Jeffrey C. Murray UofI		
	The University of Iowa		
	Department of Pediatrics, Iowa City, IA 52242, USA		
	Tel: (319) 356-3508		
	Fax: (319) 356-3347		
	Email: jeff-murray@uiowa.edu		
	Primer A: AGACTTGTAAAGATGCGTCGC		
	Primer B: GAATATTTCTGCAGTCGGA		
	STS size: 105		
	PCR Profile:		
	denature: 30 seconds at 94 degrees C		
	annealing: 75 seconds at 55 degrees C		
	extension: 15 seconds at 72 degrees C		
	PCR cycles: 27		
	extension: 6 minutes at 72 degrees C		
Protocol:			
	Template: 30ng genomic DNA		
	Primer: each 1.5 pmole		
	dNTPs: each 200 uM		
	Taq Polymerase: 0.3 units		
	Total Vol: 10 ul		
Buffer:			
	MgCl2: 1.5mM		
	KCl: 50mM		
	Tris: 10mM		
	pH: 8.3		
FEATURES			
source	Equivalent set: GATA21C11 GATA21D12 GCAL11C11		GTAT1A10 ATASAO8
	ATC6.		GCT14A05 GCAA3A07
	AFR39G03		
	location/Qualifiers		
	1..314		
	/Organism="Homo Sapiens"		
STS	54...158		
primer_bind	54...75		
primer_bind	complement(139..158)		
BASE COUNT	72 a 87 c 46 g 102 t		7 others
ORIGIN			
Query Match	2.0%; Score 32; DB 197; Length 314;		
Best Local Similarity 100.0%; Pred. No. 1.07e-16;			
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	73	ggccatcatcatcatcatcatcatcatcatca 104	
Oy	4	GGCATCATCATCATCATCATCATCATCATCTCA 35	

LOCUS	10	G09253	377 bp	DNA	STS		14-AUG-1995
DEFINITION		human STS CHLC.ATC2F09.P7509 clone ATC2F09.					
ACCESSION		G09253					
NID		g941102					
KEYWORDS		STS sequence; primer; sequence tagged site.					
SOURCE		human vector-pUCPI host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates					
ATTNORS		Catarrhini; Homnidae; Homo.					
TITLE		1 (bases 1 to 377)					
JOURNAL		Murray,J., Sheffield,V., Weber,J.L., Duyk,G. and Buetow,K.H.					
COMMENT		Cooperative Human Linkage Center Unpublished (1995) Synonyms: ATC2F09, CHLC.ATC2F09.T7508 Contact: Dr. Jeffrey C. Murray Doi					
		The University of Iowa Department of Pediatrics, Iowa City, IA 52242, USA Tel.: (319) 356-3508 Fax: (319) 356-3347 Email: jeff-murray@uiowa.edu					
		Primer A: ACCAAGCACTGAGTCCAGAG Primer B: CTGACTCCAGACCTCGTT STS size: 164 PCR Profile:					
		denature: 30 seconds at 94 degrees C annealing: 75 seconds at 55 degrees C extension: 15 seconds at 72 degrees C PCR cycles: 27 extension: 6 minutes at 72 degrees C					
		Protocol: Template: 30ng genomic DNA Primer: each 1.5 pmole dNTPs: each 200 uM Tag Polymerase: 0.3 units Total Vol: 10 ul					
		Buffer: MgCl2: 1.5mM KCl: 50mM Tris: 10mM PH: 8.3. Location/Qualifiers 1..377 /organism="Homo sapiens"					
FEATURES		source					
STS		primer_bind					
		44..207					
BASE COUNT		74 a 90 c 90 g 105 t 18 others					
ORIGIN							
		Query Match 2.0%; Score 31; DB 197; Length 377; Best Local Similarity 80.0%; Pred.No. 3,44e-15;					
		Matches 48; Conservative 0; Mismatches 11; Indels 1; Gaps 1;					
Db		91 ccacatcatcattatcatatcatatcatatcatcatcatcatcatctgttcgttgta 150					
Oy		6 CCATCATCATCATCATCATCATCATCATCA-CAGCACGGGCCATATTCAGACGACGACA 64					
RESULT	11	ATTST1025 514 bp RNA EST 13-AUG-1993					
LOCUS		DEFINITION A.thaliana transcribed sequence; clone GBGe87.					
ACCESSION		Z25512					
NID		g396648					
KEYWORDS		expressed sequence tag; partial cdna sequence.					

SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotes; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Caperales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 514)
AUTHORS Quigley and Maché, R.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1993) CNRS, GDR-1003 ACS, INRA, Laboratoire de
Biologie Moléculaire, BP 27, 31326 Castanet-Tolosan cedex, France.
E-mail: gdt-sy@toulouse.inra.fr. On behalf of: CNRS URA 1178,
Laboratoire de Biologie Moléculaire végétale, B.P. 53X, 38041
Grenoble Cedex, France. E-mail: FOUIGHEY@grenet.fr
2 (bases 1 to 514)
REFERENCE CNRS.
AUTHORS The Arabidopsis thaliana transcribed genome: the GDR cDNA program
TITLE Unpublished
JOURNAL Cloning vector: Lambda ZAP11.;
COMMENT full automatic.
FEATURES
source Location/Qualifiers
1..514
/organism="Arabidopsis thaliana"
/clone="GB8687"
/tissue_type="Flower buds of A.thaliana ecotype columbia
C24"
/clone_lib="Grenoble-B"
BASE COUNT 153 a 101 c 114 g 146 t
ORIGIN
Query Match 2.0%; Score 31; DB 19; Length 514;
Best Local Similarity 97.0%; Pred. No. 3,44e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 431 atcattcatcatcatcatcatcatcatca 463
|||||
OY 8 ATCATCATCATCATCATCATCATCATCA 40
RESULT 12
LOCUS HUMUT7996 521 bp DNA STS 28-DEC-1994
DEFINITION Human STS UT7996.
ACCESSION L30172
NID 9605349
KEYWORDS PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; trinucleotide repeat.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,
Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
White, R.
TITLE Genetic and physical mapping of simple sequence repeat containing
sequence tagged sites from the human genome
JOURNAL Unpublished (1994)
COMMENT Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: ATTCCCGGCTTGGCCGC
Primer B: GAAGAAATGTCCTCATCATG
End to Label: Primer B
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 5 94
C 10 sec. 64 C 10 sec. 72 C 20 sec. 30
58 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 1.
Location/Qualifiers

source 1..521
/organism="Homo sapiens"
STS 151..328
/standard_name="STS UT7996"
primer_bind 151..169
/evidence=experimental
primer_bind complement(308..328)
/evidence=experimental
BASE COUNT 103 a 163 c 103 g 143 t 9 others
ORIGIN
Query Match 2.0%; Score 32; DB 205; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.07e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 207 gccatcatcatcatcatcatcatcatca 238
|||||
OY 4 GGCATCATCATCATCATCATCATCATCA 35
RESULT 13
LOCUS HUMUT7996 521 bp DNA STS 28-DEC-1994
DEFINITION Human STS UT7996.
ACCESSION L30172
NID 9605349
KEYWORDS PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; trinucleotide repeat.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,
Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
White, R.
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JOURNAL Unpublished (1994)
COMMENT Submitted by: Utah Center for Human Genome Research University of
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2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: ATTCCCGGCTTGGCCGC
Primer B: GAAGAAATGTCCTCATCATG
End to Label: Primer B
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 5 94
C 10 sec. 64 C 10 sec. 72 C 20 sec. 30
58 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 1.
FEATURES
source Location/Qualifiers
1..521
/organism="Homo sapiens"
STS 151..328
/standard_name="STS UT7996"
primer_bind 151..169
/evidence=experimental
primer_bind complement(308..328)
/evidence=experimental
BASE COUNT 103 a 163 c 103 g 143 t 9 others
ORIGIN
Query Match 2.0%; Score 32; DB 204; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.07e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 207 gccatcatcatcatcatcatcatcatca 238
|||||
OY 4 GGCATCATCATCATCATCATCATCATCA 35

MORSE
(TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Apr 25 12:04:26 1997; MasPar time 9.19 Seconds
Tabular output not generated.
583.635 Million cell updates/sec

Title: >US-08-699-716A-2
Description: (1-521) from US08699716A.pep
Perfect Score: 3546
Sequence: 1 MGNHHHHHHHSSGHIDD.....RFIOKYSVMORLLDITSGK 521

Scoring table:
PAM 150
Gap 11

Searched: 88003 segs, 10295656 residues

Post-Processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 35.391; Variance 190.955; scale 0.185

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2242	63.2	329 15	R79961	Partial LcrV (V anti	3.48e+164
2	2233	63.0	329 15	R79962	Partial LcrV (V anti	1.80e+163
3	1100	31.0	170 14	R76528	Yersinia pestis cal	5.61e-74
4	968	27.3	151 14	R76526	Yersinia pestis cal	1.17e-63
5	966	27.2	151 14	R76527	Yersinia pestis cal	1.67e-63
6	150	4.2	462 17	R95009	Type A neurotoxin C f	3.06e-02
7	110	3.1	835 17	R96206	Invasin protein.	9.84e+00
8	106	3.0	174 10	R88503	Borrelia burgdorferi	1.70e+01
9	108	3.0	455 10	R57771	Borrelia burgdorferi	1.30e+01
10	105	3.0	493 3	R13992	Mouse nucleodindin.	1.95e+01
11	106	3.0	708 2	R08402	Amli105 encoded by Ida	1.70e+01
12	106	3.0	2482 14	R72826	Human mitosis.	1.95e+01
13	105	3.0	3248 18	R99795	Kinetochore protein C	2.55e+01
14	103	2.9	257 7	R36675	30 kD Borrelia burgdo	1.95e+01
15	103	2.9	563 3	R13139	B.burgdorferi strain	2.55e+01
16	102	2.9	1529 18	R97965	CORR potassium channe	4.36e+01
17	99	2.8	793 4	R31216	Penicillin binding pr	3.82e+01
18	100	2.8	793 4	R20743	Murine receptor type	3.82e+01
19	100	2.8	793 18	W02282	Murine receptor type	3.82e+01
20	100	2.8	802 18	W02283	Human receptor type p	3.82e+01
21	100	2.8	802 4	R20744	Human receptor type p	3.82e+01

22	99	2.8	3567	8	R44431	eryA region polypepti	4.36e+01
23	96	2.7	183	14	R74640	PRRS virus (Spanish s	6.48e+01
24	96	2.7	183	17	R94724	PRRSV Lelystad ORF-4	6.48e+01
25	96	2.7	183	17	R88704	Porcine reproductive	6.48e+01
26	96	2.7	183	6	R29943	Deduced from Lelystad	6.48e+01
27	97	2.7	302	15	R82097	Human Gax protein.	5.68e+01
28	97	2.7	303	15	R82096	Ret Gax protein.	5.68e+01
29	96	2.7	350	4	R20230	hGox-1.	6.48e+01
30	97	2.7	414	6	R32020	Sequence of a eukaryo	5.68e+01
31	96	2.7	423	16	R89408	Stress activated prot	6.48e+01
32	95	2.7	652	2	R08403	Amli105 encoded by Mas	7.39e+01
33	95	2.7	924	3	R10889	Leukotoxin 352 encode	7.39e+01
34	95	2.7	924	8	R42385	Recombinant leukotoxi	7.39e+01
35	95	2.7	926	10	R14482	LKT352.	7.39e+01
36	95	2.7	926	10	R50291	Recombinant leukotoxi	7.39e+01
37	95	2.7	936	7	R34547	GHRH-leukotoxin gene	7.39e+01
38	95	2.7	953	11	R60072	PKA protein of Paste	7.39e+01
39	95	2.7	953	3	R15159	Leukotoxin from P. ha	7.39e+01
40	95	2.7	1069	9	R52748	Bovine IFNgamma/LKT c	7.39e+01
41	97	2.7	1098	4	R22103	Bovine IL-2 - LKT fus	5.68e+01
42	95	2.7	1098	9	R52747	Bovine IL-2/LKT chime	7.39e+01
43	95	2.7	1267	1	R04232	Rickettsia rickettsii	7.39e+01
44	96	2.7	1338	8	R41731	High molecular weight	6.48e+01
45	95	2.7	1427	2	R10534	Human 160kD mediator	7.39e+01

ALIGNMENTS

RESULT 1
ID R79961 standard; Protein: 329 AA.

AC R79961,
DE 18-APR-1996 (first entry)
KW Partial LcrV (V antigen) of Y. pestis.
OS LcrV; V antigen; virulence; plague; vaccine; epitope.
PN Yersinia pestis.
MO9524475-A1.
PD 14-SEP-1995.
PE 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA) UK SEC FOR DEFENCE.
PI Leary SEC, Titball RW, Williamson ED, Leary SE;
DR WPI, 95-328268/42.
N-PSDB; T04222.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
oral or parenteral vaccines for protection against plague
PS Claim 6: Page 11-13: 25pp; English.
CC R79961-62 are encoded by T04222-23 (resp.), DNA sequences (LcrV) encoding
all or a protective epitopic part of the mature V protein of Yersinia
CC pestis. The protein was expressed as a fusion protein with maltose
CC binding protein or glutathione-S-transferase in 3 different plasmid
CC vectors. Y. pestis is the highly virulent causative organism of plague
CC in a wide range of animals, including man. The V antigen (LcrV) is an
CC unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid.
CC The V antigen is postulated to act as a virulence antigen, and
CC transformed microorganisms contg. recombinant DNA encoding a V antigen
CC protein/peptide are useful in vaccines to protect against plague.
SQ Sequence 329 AA:

Query Match 63.2%; Score 2242; DB 15; Length 329;
Best Local Similarity 99.4%; Pred. No. 3.48e+164;
Matches 326; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Db 3 ef-iryeqnpqhfiadlekvrveqtlthqssvleelvtqkdnidiskvprkxse 61
11 |||||
Qy 194 EFMRIRAYEQPHFIDLEKVRVEQTLTHQSSVLEELVLTQKKNIDISKVPRKDS 253
194 FANRVITDDIELKRLAFLPEDITLKGHYDNLONGIKRKEFLSSPNTQWELRAF 313
Qy 62 fanrvitddielkrlayfipedaalkgghydnqngkrykveflsspnqtwelraf 121
11 |||||
Db 122 mavmhsitadridddilivvsgmhbdarskrlaeaeltaelklysvgaeeinkh 181
11 |||||
Qy 314 MAVMHSITADRIDDDILKLYVDSNMHGDARSKRLAEELTAELKLYSVIOAEINKH 373

Db 182 sssgtinhdksinlmdknlgygtdeefkaseaykilekmpgttiqvgsekkivskd 241
|||||
QY 374 SSSGTINHDKSNLMDKNLGYGTDEEIRKASAEYKILEKMPGTTIQVGSEKKIVSIND 433
Db 242 ffgsenkrtgalgnknsysynkdneshfctscdskrplndlvsgkttqtsdtsrf 301
|||||
QY 434 ffgsenkrtgalgnknsysynkdneshfctscdskrplndlvsgkttqtsdtsrf 493
Db 302 nsaealnrfiikkydsvmgrliddtsqk 329
|||||
QY 494 NSAEALNRFIOKRYDSVMORLDDTSQK 521

RESULT 2
ID R79962: standard; Protein: 329 AA.
AC R79962: 18-APR-1996 (first entry)
DE Partial lcrv (V antigen) of Y. pestis.
KW lcrv; V antigen; virulence; plague; vaccine; epitope.
OS Yersinia pestis.
PN WO9524475-A1.
PD 14-SEP-1995.
PF 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA) UK SEC FOR DEFENCE.
PI Leary SEC, Titball RW, Williamson ED, Leary SE;
DR WPI: 95-328268/42.
DR N-PSDB: T04223.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
oral or parenteral vaccines for protection against plague
PS Claim 6; Page 15-16; 25pp; English.
CC R79961-62 are encoded by T04223-23 (resp.), DNA sequences (lcrv) encoding
all or a protective epitopic part of the mature V protein of Yersinia
pestis. The protein was expressed as a fusion protein with maltose
binding protein or glutathione-S-transferase in 3 different plasmid
vectors. Y. pestis is the highly virulent causative organism of plague
in a wide range of animals, including man. The V antigen (lcrv) is an
unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb lcr plasmid.
CC The V antigen is postulated to act as a virulence antigen, and
transformed microorganisms contg. recombinant DNA encoding a V antigen
CC protein/peptide are useful in vaccines to protect against plague.
SQ Sequence 329 AA;

Query Match 63.0%; Score 2233; DB 15; Length 329;
Best Local Similarity 99.4%; Pred. No. 1.80e-163;
Matches 323; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 5 itayeqnpgfhiedlekvrveqltghssvleelvglvkdknidisikydpkxsevfaf 64
|||||
QY 197 IRAYEQNPQHFIEDLEKVRVEQLTGHSSVLEELVQLVYKDNIDISIKYDPKXSEVFAN 256
Db 65 rvtlddelikklilayfipedaalkghydnqlngikrvkeflesspntqwelirafmay 124
|||||
QY 257 RVTLDIELIKKILAFLEPEDIKRGHYDNOLONGIKRKEPLESSPNTQWELIRAFMAY 316
Db 125 mhfsitadriiddllkviydsmdmhgdarskireelaqitlaeklysvigaelnkhlss 184
|||||
QY 317 MHFSITADRIIDDILKVIYDSMDMHGDARSKIREELAEITAEIKYISVQAEINKHLSSS 376
Db 185 gfinhdkseinlmdknlgygtdeefkaseaykilekmpgttiqvgsekkivskd 244
|||||
QY 377 GFINHDKSINLMDKNLGYGTDEEIRKASAEYKILEKMPGTTIQVGSEKKIVSIND 436
Db 245 senkrtgalgnknsysynkdneshfctscdskrplndlvsgkttqtsdtsrf 304
|||||
QY 437 SENKRTGALGNKNSYSYNKDNESHFATCSDKSRPLNDLVSGKTTQTSDFNSA 496
Db 305 lealnrfiikkydsvmgrliddtsqk 329
|||||
QY 497 LEALNRFIOKRYDSVMORLDDTSQK 521

RESULT 3
ID R76528: standard; Protein: 170 AA.
AC R76528: 17-DEC-1995 (first entry)
DE Yersinia pestis cafi (F1) antigen.
KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KW bubonic plague; pneumonic plague.
OS Yersinia pestis.
PN WO9518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI: 95-246396/32.
DR N-PSDB: Q92819.
PT DNA constructs capable of transforming microorganisms - which can be
used as live or attenuated vaccines which induce an immune response,
against Yersinia pestis, at mucosal surfaces.
PS Disclosure: Page 20; 27pp; English.
CC The sequence represents the Y. pestis cafi (F1) antigen expressed
from plasmid pF0RFB. The DNA construct can be used to transform
human or animal gut colonizing microorganisms, specifically
attenuated Salmonella typhimurium or Salmonella typhi. The
transformed microorganisms can be used as live/attenuated vaccines
CC which induce immune responses at mucosal surfaces. The vaccines
provide protection against infection with Y. pestis, and are
parenterally and orally active vaccines offering protection
CC against bubonic and pneumonic plague.
SQ Sequence 170 AA;

Query Match 31.0%; Score 1100; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.61e-74;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mkhissvialafglatanaadlastatatlvepariltlykegapitmdnqndt 60
|||||
QY 24 MKHISSVIALAFGLATANADLASTATATVEPARILTLYKEGAPITMDNGNIDT 83
Db 61 ellvgtlclgykctttsvntftdaagdmnylittsgdgmnhqfctkvigkdsrddis 120
|||||
QY 84 ELLVGTLC LGYKCTTTSVNTFTDAAGDMNYLITTSQDGMNHQFCTKVIGKDSRDPDIS 143
Db 121 pkvngenlygdgvlatysqgdfvrsigskgkllaakrytdavtyvnsq 170
|||||
QY 144 PKVNGENLYGDDVVLATGSQDFVRSISGSKGLAAGKITDAVTVTSNQ 193

RESULT 4
ID R76526: standard; Protein: 151 AA.
AC R76526: 17-DEC-1995 (first entry)
DE Yersinia pestis cafi (F1) antigen.
KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KW bubonic plague; pneumonic plague.
OS Yersinia pestis.
PN WO9518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI: 95-246396/32.
DR N-PSDB: Q92817.
PT DNA constructs capable of transforming microorganisms - which can be
used as live or attenuated vaccines which induce an immune response,
against Yersinia pestis, at mucosal surfaces.
PS Disclosure: Page 16; 27pp; English.
CC The sequence represents the Y. pestis cafi (F1) antigen expressed
from plasmid pF0AL2a. The DNA construct can be used to transform
human or animal gut colonizing microorganisms, specifically
attenuated Salmonella typhimurium or Salmonella typhi. The
transformed microorganisms can be used as live/attenuated vaccines

CC which induce immune responses at mucosal surfaces. The vaccines
CC provide protection against infection with Y. pestis, and are
CC parenterally and orally active vaccines offering protection
CC against bubonic and pneumonic plague.
SQ Sequence 151 AA;

Query Match 27.3%; Score 968; DB 14; Length 151;
Best Local Similarity 96.0%; Pred. No. 1.17e-63;
Matches 148; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 ssadlstatatatlveparititykegapitlmdngnidellvgtllygkytqtst 60
QY 43 NAADLTATATATATVEPARITITLTKKCAPITIMDNGNIDELLVGTLYGKYTQTST 102
Db 61 vnftdaagdpmylftfsgqgnbqfttkvlgksrdldispkngenvlgddvlatgs 120
QY 103 SVNFTDAAGDPMYLFTFSQGNHNOFTTKVYLGKSRDLDISPKNGENLVGDVVLATGS 162
Db 121 qdftvrsigsgkylaaqkytdavtvtsnq 151
QY 163 QDEFFVRSIGSGKGLAAQKYTDVTVTSNQ 193

RESULT 5

ID R76527 standard; Protein; 151 AA.
AC R76527;
DT 17-DEC-1995 (first entry)
DE Yersinia pestis cafI (F1) antigen.
KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KM bubonic plague; pneumonic plague.
OS Yersinia pestis.
PN W09518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC. FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Tithball RW, Williamson ED;
DR WPI; 95-246396/32.
DR N-PSDB; Q92818.
PT DNA constructs capable of transforming microorganisms - which can be
PT used as live or attenuated vaccines which induce an immune response,
PT against Yersinia pestis, at mucosal surfaces.
PS Disclosure; Page 18; 27pp; English.
CC The sequence represents the Y. pestis cafI (F1) antigen expressed
CC from plasmid pF132a. The DNA construct can be used to transform
CC human or animal gut colonizing microorganisms, specifically
CC attenuated Salmonella typhimurium or Salmonella typhi. The
CC transformed microorganisms can be used as live/attenuated vaccines
CC which induce immune responses at mucosal surfaces. The vaccines
CC provide protection against infection with Y. pestis, and are
CC parenterally and orally active vaccines offering protection
CC against bubonic and pneumonic plague.
SQ Sequence 151 AA;

Query Match 27.2%; Score 966; DB 14; Length 151;
Best Local Similarity 96.7%; Pred. No. 1.67e-63;
Matches 148; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 padltatatatlveparititykegapitlmdngnidellvgtllygkytqtst 61
QY 44 AADLTATATATATVEPARITITLTKKCAPITIMDNGNIDELLVGTLYGKYTQTST 103
Db 62 vnftdaagdpmylftfsgqgnbqfttkvlgksrdldispkngenvlgddvlatgs 121
QY 104 VNFTDAAGDPMYLFTFSQGNHNOFTTKVYLGKSRDLDISPKNGENLVGDVVLATGSQ 163
Db 122 dftvrsigsgkylaaqkytdavtvtsnq 151
QY 164 DFFVRSIGSGKGLAAQKYTDVTVTSNQ 193

RESULT 6
ID R95009 standard; Protein; 462 AA.

AC R95009;
DT 07-JUL-1996 (first entry)
DE Type A neurotoxin C fragment-polystyridine tag fusion pHisBot.
KW Toxin; neurotoxin; fusion protein; antitoxin; vaccine; immunogen;
KM Clostridium botulinum; polystyridine; vector; pPTHisa; pHisBot.
OS Synthetic.

FT Key Location/Qualifiers
FT Peptide 1..21
FT /label= Polystyridine-tag
FT Protein 22..462
FT /label= C-fragment
PN W09612802-A1.
PD 02-MAY-1996.
PF 23-OCT-1995; U13737.
PR 24-OCT-1994; US-329154.
PR 16-MAR-1995; US-405496.
PR 14-APR-1995; US-422711.
PR 07-JUN-1995; US-480604.
PA (OPH-) OPHIDIAN PHARM INC.
PI Firca JR, Kink JA, Padhye NV, Stafford DC, Thalley BS;
PI Williams JA;
DR WPI; 96-230603/23.
DR N-PSDB; T29246.

PT Fusion proteins comprising non-toxin protein and part of toxin -
PT useful to form anti-toxins against Clostridium botulinum type A, and
PT C. difficile type toxins, and to treat C. difficile intoxication,
PT paritc. diarrhoea
PS Claim 7; Page 340-342; 434pp; English.
CC phisbot fusion protein (R95009), the product of a nucleotide
CC sequence (T29246) in vector pPTHisa, comprises a polystyridine
CC affinity tag and fragment C (see also R95008) of the Clostridium
CC botulinum type A neurotoxin. The phisbot protein was expressed
CC in Escherichia coli as a soluble protein and was purified by
CC metal chelate affinity chromatography to obtain a product free
CC of endotoxin contamination that may be useful as an immunogen
CC in vaccine compns.
SQ Sequence 462 AA;

Query Match 4.2%; Score 150; DB 17; Length 462;
Best Local Similarity 59.4%; Pred. No. 3.06e-02;
Matches 19; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

Db 1 mgnhhhhhhhhsghleg--rhmasmarlls 30
QY 1 MGNHHHHHHHSSGHIDDDKMKKISSYIA 32

RESULT 7

ID R96206 standard; Protein; 835 AA.
AC R96206;
DT 24-AUG-1996 (first entry)
DE Invasin protein.
KW Invasin; drug delivery; gastrointestinal membrane; transcytosis;
KW bioavailability; fusion protein; enterocyte; Peyers patch M-cell.
OS Yersinia enterocolitica strain 8081c.
FH Key Location/Qualifiers
FT Region 645..835
FT /note= "C-terminal receptor binding region"
PN W09613250-A1.
PD 09-MAY-1996.
PF 20-OCT-1995; U13749.
PR 27-OCT-1994; US-331393.
PA (AMGE-) AMGEN INC.
PI Habbelfield AD, Jensen-Piippo K;
DR WPI; 96-251447/25.
DR N-PSDB; T27535.
PT Therapeutic delivery system utilising bacterial invasin protein - is
PT not readily degraded in the gut, enhances systemic bio-availability
PT of therapeutic agents
PS Example 1; Fig 1; 110pp; English.
CC The sequence represents a bacterial invasin protein, which may be
CC complexed with a therapeutic agent to transport the agent across
CC the gastrointestinal membrane barrier by transcytosis to increase

1
2
3
4

5


```
|||||
Oy 496 AIEALNRFIOKYDSVMORLLDPTSGK 521

RESULT 2
ENTRY B37314 #type complete
TITLE regulatory protein LcrV - Yersinia pseudotuberculosis
ORGANISM #formal_name Yersinia pseudotuberculosis
DATE 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change
17-Feb-1994

ACCESSIONS B37314
REFERENCE A37314
#authors Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.;
#journal Maccellaro, A.; Baeckman, A.; Boelin, I.; Wolf-Watz, H.
#title J. Bacteriol. (1991) 173:1607-1616
Analysis of the V antigen lcrGVH-yopBD operon of Yersinia
pseudotuberculosis: evidence for a regulatory role of LcrV
and LcrV.

#accession B37314
#status Preliminary
#molecule_type DNA
#residues 1-326 #label BER
#cross-references GB:M57893
SUMMARY #length 326 #molecular-weight 37336 #checksum 4689

Query Match 61.8%; Score 2192; DB 9; Length 326;
Best Local Similarity 96.6%; Pred. No. 2,08e-274;
Matches 315; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 1 mlrayerqpnqfiedlekveqlcgshsvleelvgqvkdknldlskypdksevf 60
Oy 196 MIRAYEQNPQHFIEDLEKRVESQILGHSSEVLELVQLVKDKNDISIKYDPRKDSYV 255
Db 61 nrvtddeellkklayflpedalkqgbydnqnglkrvvefllessntqwellrafna 120
Oy 256 NKVITDDLELKKILAYFEPEDTILKGCHYDQLONGIKRVEFLESSNTQWELRAFNA 315
Db 121 vhfsltdridddllkvvdsnmhgdarskrelaeltaelkkyvsgaelnkhss 180
Oy 316 VMHFSUTADRIDDDILKIVYDSNMHGDARSKRELAEITAELEKITYSTQLEFNKHSS 375
Db 161 gctlnhdkslnlmcknljyvtdeefkasaeykilekmpqtllegeetkivsknfl 240
Oy 376 SGTINIHDKSIMLMDKNLGYTDEEFKASAEYKILEKMPQTTQVDSSEKTIYSIKDEL 435
Db 241 esekrrtgalglnkdsysynkhneshatccsksrplnlvsgktqgldtsrfs 300
Oy 436 GSENRRTGALGMLKNSYSYNKDNELSHPATYCSKSRPLNLVSOKTQLSDITSRFS 495
Db 301 alealnrfiqkydsymgrllldtsgk 326
Oy 496 AIEALNRFIOKYDSVMORLLDPTSGK 521

RESULT 3
ENTRY S13008 #type complete
TITLE capsular antigen Fl precursor - Yersinia pestis
ORGANISM #formal_name Yersinia pestis
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
18-Jun-1993
ACCESSIONS S13008; S23725
REFERENCE S13008
#authors Galyov, E.E.; Smirnov, O.Y.; Karlishhev, A.V.; Volkovoy, K.I.;
Denesyuk, A.I.; Nazimov, I.V.; Rubtsov, K.S.; Abramov,
V.M.; Dalvadpazanz, S.M.; Zav'yalov, V.P.
#journal FEBS Lett. (1990) 277:230-232
#title Nucleotide sequence of the Yersinia pestis gene encoding Fl
antigen and the primary structure of the protein. Putative
T and B cell epitopes.
#cross-references MUID:91099503
#accession S13008
#molecule_type DNA
#residues 1-170 #label GAL
```

```
##cross-references EMBL:X61996
GENETICS
#gene cafi
FEATURE 1-21
22-170
SUMMARY #length 170 #molecular-weight 17666 #checksum 5455

Query Match 31.0%; Score 1100; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.88e-124;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mkksvtaiaalfgtatanaadttaattataveparitlykegapitmdnqndt 60
Oy 24 MKKISSVIAIALFGITANANADLTASTATATVLEPARITLYTKEGAPITMDNGNIDT 83
Db 61 ellvgtlcggkigttsvntfdaagdpmlylftsgdgnbqftkviqkdsrdids 120
Oy 84 ELVGTLTLLGGYKGTGTSTVNTFDAQDPMYLTFTSGDGNBQFTTRKVIKDSRDIS 143
Db 121 pkvngenvlgddvylatgsqdfivrjsksgkilaagkytavrvtvsng 170
Oy 144 PKVNGENVLGDDVYLATGSQDFIVRSIGSKGKTLAAGKYTDAVTAVTYSNQ 193

RESULT 4
ENTRY I58315 #type complete
TITLE WT1 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996

ACCESSIONS I58315
REFERENCE I58315
#authors Hamilton, T.B.; Barilla, K.C.; Romanjuk, P.J.
#journal Nucleic Acids Res. (1995) 23:277-284
#title High affinity binding sites for the Wt1ms' tumour suppressor
protein WT1.
#cross-references MUID:95166649
#accession I58315
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-168 #label RES
#cross-references GB:S75264; NTD:9896246; CDS_PID:9896247
GENETICS
#note gene name WT1
SUMMARY #length 168 #molecular-weight 20165 #checksum 6457

Query Match 4.7%; Score 168; DB 13; Length 168;
Best Local Similarity 66.7%; Pred. No. 4.08e-05;
Matches 20; Conservative 7; Mismatches 1; Indels 2; Gaps 1;

Db 1 mgbbhhhhhhhsqhgleg--rhmrtypgv 28
Oy 1 MGHNNHHHHHSSCHIDDDKHMKKISSV 30

RESULT 5
ENTRY S07904 #type complete
TITLE CS3 pilin precursor - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
ACCESSIONS S07904
REFERENCE S07904
#authors Jajlajakumari, M.B.; Thomas, C.J.; Halter, R.; Manning, P.A.
#journal Mol. Microbiol. (1989) 3:1685-1695
#title Genes for biosynthesis and assembly of CS3 pilin of CFA/II
enterotoxigenic Escherichia coli: novel regulation of pilus
production by bypassing an amber codon.
#cross-references MUID:90158116
#accession S07904
#status preliminary
```

##molecule-type DNA
##residues 1-168 ##label JAL
##cross-references EMBL:X16944
SUMMARY #length 168 #molecular-weight 17491 #checksum 8973

Query Match 3.6%; Score 127; DB 9; Length 168;
Best Local Similarity 24.1%; Pred. No. 3,73e-01;
Matches 41; Conservative 47; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlkiky11glsamsyslaaagptlkelaInvlspsaalatwpaqdnltntg-v 59
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
24 MKRISV-IAIALFGTIA-TANADLFASTATATVEPARITLYKEGAPITMDNGNI 81
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 60 -snltvgvltlntsidtvsiasstskngt-vtfahetnsafatc-istdani 116
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Qy 82 DTELVLGTLTGKTKGTTS-TSVNFTDAAGDPMYLFTFSQDGNHGFYTKVIGKDSRDF 140
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 117 tld-knagntiv-ktngsqplnplkfttgnenhlysgnyranltt 164
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Qy 141 DISPKVNGENLVGDVYLVATGSODFEVRSIGSKGK-LAAGKTYDAVT 189
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
RESULT 6
ENTRY S57382 #type complete
TITLE hypothetical protein YOL087c - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein O0944
ORANISM formal_name Saccharomyces cerevisiae
DATE 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 02-Aug-1996
ACCESSIONS S57382; S66781; S50418
REFERENCE S57374
#authors Zumbstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
#journal Yeast (1995) 11:975-986
#title A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.
#accession S57382
#status nucleic acid sequence not shown
#molecule-type DNA
##residues 1-1116 ##label ZUM
##cross-references EMBL:X83121
REFERENCE S66775
#authors Zumbstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
#submission submitted to the Protein Sequence Database, July 1996
#accession S66781
#molecule-type DNA
##residues 1-1116 ##label ZUM
##cross-references EMBL:Z74829
#experimental_source strain S288C
GENETICS
#map-position 15L
SUMMARY #length 1116 #molecular-weight 125381 #checksum 1996

Query Match 3.6%; Score 127; DB 11; Length 1116;
Best Local Similarity 47.1%; Pred. No. 3,73e-01;
Matches 16; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Db 365 hhhhhheegnistdtkvkkvggldlaal 398
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Qy 3 HHHHHHHHSSGHDDDKMKKISSVIAIALF 36
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
RESULT 7
ENTRY A34952 #type complete
TITLE CS3 fimbrial protein precursor - Escherichia coli
ORANISM formal_name Escherichia coli
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 04-Nov-1994
ACCESSIONS A34952
REFERENCE A34952

#authors Boylan, M.; Smyth, C.J.; Scott, J.R.
#journal Infect. Immun. (1988) 56:3297-3300
#title Nucleotide sequence of the gene encoding the major subunit of CS3 fimbriae of enterotoxigenic Escherichia coli.
#cross-references MIMD:89032631
#accession A34952
##molecule-type DNA
##residues 1-168 ##label BOY
##cross-references GB:M35657
FEATURE
1-15 #domain (or 1-22) signal sequence #status predicted
16-168 #label SIG
#product (or 17-168) CS3 fimbrial protein #status predicted #label MAT
SUMMARY #length 168 #molecular-weight 17464 #checksum 9103

Query Match 3.5%; Score 123; DB 9; Length 168;
Best Local Similarity 23.5%; Pred. No. 8.48e-01;
Matches 40; Conservative 48; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlkiky11glsamsyslaaagptlkelaInvlspsaalatwpaqdnltntg-v 59
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Qy 24 MKRISV-IAIALFGTIA-TANADLFASTATATVEPARITLYKEGAPITMDNGNI 81
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 60 -snltvgvltlntsidtvsiasstskngt-vtfahetnsafatc-istdani 116
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Qy 82 DTELVLGTLTGKTKGTTS-TSVNFTDAAGDPMYLFTFSQDGNHGFYTKVIGKDSRDF 140
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 117 tld-knagntiv-ktngsqplnplkfttgnenhlysgnyranltt 164
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Qy 141 DISPKVNGENLVGDVYLVATGSODFEVRSIGSKGK-LAAGKTYDAVT 189
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
RESULT 8
ENTRY S47608 #type complete
TITLE actin homolog YOL081c - Yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein J1012; protein YOL081c
ORANISM formal_name Saccharomyces cerevisiae
DATE 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 08-Sep-1995
ACCESSIONS S47608; S56029; S56858; S37563
REFERENCE S47608
#authors Wintersberger, U.
#submission submitted to the EMBL Data Library, December 1993
#accession S47608
#molecule-type DNA
##residues 1-489 ##label WIN
##cross-references EMBL:X75317
REFERENCE S56016
#authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Chaiwatizis, N.; Baur, A.; Boles, E.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Zimmermann, F.K.
#journal Yeast (1995) 11:681-689
#title Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)(2)-Cys(6) binuclear cluster domain and a putative alpha-2-SCB-alpha-2 binding site.
#accession S56029
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
##residues 1-489 ##label MIO
##cross-references EMBL:X83502
#note the nucleotide sequence was submitted to the EMBL Data Library, December 1994
REFERENCE S56855
#authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chaiwatizis, N.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Witzel, A.; Zimmermann, F.K.
#submission submitted to the Protein Sequence Database, September 1995
#accession S56858
##molecule-type DNA
##residues 1-489 ##label MIW

GENETICS		#cross-references EMBL:449356	
#gene	ACT3		
#map_position	10L		
CLASSIFICATION	#superfamily actin		
SUMMARY	#length 489 #molecular-weight 54831 #checksum 8019		
Query Match			
Best Local Similarity	3.5%; Score 123; DB 7; Length 489;		
Matches	16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;		
Db	22 gsytnlgyssdfpsilpvygkytaedgnkklfsgsglprdkyellplie-nglv 80		
Qy	93 GGRKGTSTSVNFTDAAGDPMTLFTFSQDNNHQFTTKVIGKSRPFDSPKNGENLV 152		
Db	81 id 82		
Qy	153 GD 154		
RESULT	9		
ENTRY	S33821	#type complete	
TITLE	median body protein - Giardia lamblia		
ORGANISM	#formal name Giardia lamblia		
DATE	06-Jan-1995	#sequence_revision 06-Jan-1995	#text_change 06-Jan-1995
ACCESSIONS	S33821		
REFERENCE	S33821		
#authors	Marshall, J.; Holberton, D.V.		
#journal	J. Mol. Biol. (1993) 231:521-530		
#title	Sequence and structure of a new coiled coil protein from a microtubule bundle in Giardia.		
#accession	S33821		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-857	#label MAR	
#cross-references	EMBL:X64517		
SUMMARY	#length 857 #molecular-weight 100583 #checksum 6805		
Query Match			
Best Local Similarity	3.5%; Score 124; DB 12; Length 857;		
Matches	43; Conservative 71; Mismatches 82; Indels 18; Gaps 17;		
Db	582 erveeerlqkekemllkqritleqgqratvretemalirekaneldynergerah 641		
Qy	205 OHFIED-LEKRVREQTLGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVEFA-NRVITD- 261		
Db	642 eimlmdalalscdklrqnryamnel-teltekvgllklyekrrardvemlelrhamd 700		
Qy	262 DIELLK-KILLYF-LPEETLILKGHYDNLONGIKRV-K-EFLSSPPTQ-WELRA-FMA 315		
Db	701 vdtlveekqrlsemrlaelikvynyddaqdakarlgelkemsdkliefemimdd-nrrl 759		
Qy	316 VMHFSLTADRIKDDDI--LKATVDSNNHNGDARSKLRELAELTALMLKTYVIAQAFIKHL 373		
Db	760 klqv-k-elldlktan-mek-lyeeykklcdqlkat 790		
Qy	374 SSSGTFINHDKSNIMDKNLGY-YTD-EIRPKAS 405		
RESULT	10		
ENTRY	S15999	#type complete	
TITLE	fatty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast		
ORGANISM	(Yarrowia lipolytica)		
DATE	#formal name Yarrowia lipolytica, Candida lipolytica		
ACCESSIONS	30-Jun-1993	#sequence_revision 30-Jun-1992	#text_change 11-Jun-1993
REFERENCE	S15999		
#authors	Koetting, H.; Rotner, G.; Beck, R.F.; Schweizer, M.; Schweizer, E.		
#journal	Mol. Gen. Genet. (1991) 226:310-314		
#title	The penicillin functional FAS1 genes of Saccharomyces cerevisiae		

and Yarrowia lipolytica are co-linear and considerably longer than previously estimated.

```
#cross-references M01D:91238709
#accession S15999
##molecule_type DNA
##residues 1-2076 ##label MOL
##cross-references EMBL:X59690

GENETICS
#gene FAS1
KEYWORDS acyltransferase
SUMMARY #length 2076 #molecular-weight 230223 #checksum 5483

Query Match      3.5%  Score 123; DB 11; Length 2076;
Best Local Similarity 31.3%; Pred.No.8.4e-01;
Matches 25; Conservative 22; Mismatches 28; Indels 5; Gaps 5

Db 1268 tdnrttikefwkllwfggdk-feldtdit-eeigddvttsgrakadfyhavgnkgeaf 1325
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 119 TSQDNQHNFQTTKY-IGKDSRDFPISRKVNGENLVGDYVLATSQDPFVRSTSKSGKL 177
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 178 AAGKTYDAVTVSNOEFMI 197

RESULT 11
ENTRY          S48450    #type complete
TITLE          hypothetical protein YIL007c - yeast (Saccharomyces cerevisiae)
ORGANISM       . #formal_name Saccharomyces cerevisiae
DATE           02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 01-Mar-1996

ACCESSIONS     S48450
REFERENCE      S48442
#authors       Rowley, N.
#submission    submitted to the EMBL Data Library, August 1994
#accession     S48450
##molecule_type DNA
##residues     1-220 ##label ROW
##cross-references EMBL:L38113

GENETICS
#map_position 9L
SUMMARY        #length 220 #molecular-weight 24846 #checksum 3126

Query Match      3.4%  Score 120; DB 11; Length 220;
Best Local Similarity 22.8%; Pred.No.1.5e+00;
Matches 34; Conservative 39; Mismatches 69; Indels 7; Gaps 7,

Db 38 ktdietgleay-fsvleqeg-tgmdsalvtpdgy-prsdvdvlgtmtlrknvmllnkndln 94
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 213 KRVRE-QLTGGSSYLEELVOLVRDKNIDISIKYDPKRDSSEVFANRYITDDIELKKILA 271
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 95 hllgrshvllnqhdehnmvknkgdaarn-nodgaigtflpfafisevvpgspedkaktkv 153
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 212 yFLPEDTTLKGCHVDNLQNIKKVKKELESPPWTQWELEA-AFMAVMHFSFLTADRIDDII 330
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 154 ddkllisignvaahnskliguigmvmkne 182
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 331 LKVIVDSNMHHGDKARSLRE-ELAEIINAE 358
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
ENTRY          KIBYRB   #type complete
TITLE          ribokinase (EC 2.7.1.15) - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein YCR036w; protein YCR533
ORGANISM       #formal_name Saccharomyces cerevisiae
DATE           31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 23-Aug-1996
ACCESSIONS     S12918; S19448
REFERENCE      S12916
#authors       Thierry, A.; Fairhead, C.; Dujon, B.
#journal       Yeast (1990) 6:521-534
#title         The complete sequence of the 8.2 kb segment left of MAT on
```


! :
QY 158 LATGSDFFV 167

Search completed: Fri Apr 25 12:04:07 1997
Job time : 83 secs.

Db 241 gseukrtcalnllkmsvynkdmelnlsfaticdsksprindlysgkttqtsatfrs 300
QY 436 GSENRITCALGNLKNSYSYNNDDNNEHLSFATTCSDKSPRLNDLVSQATTDLSDTTSFNS 495
Db 301 aiealnfrfkygswmgrrlldtsgx 326
QY 496 AIEALNFRITQKIDSVMORLDDTSGK 521

RESULT	2	STANDARD;	PRT;	326 AA.
ID	ICRV YERPS			
AC	P23994;			
DT	01-MAR-1992 (REL. 21, CREATED)			
DT	01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)			
DT	01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)			
DE	VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN V).			
GN	ICRV.			
OS	YERSINIA PSEUDOTUBERCULOSIS.			
OG	PLASMID PIB1.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
CC	ENTEROBACTERIACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-YPIII;			
RC	MEDLINE; 91154114.			
RA	BEGGMAN T., HAKANSSON S., FORSBERG A., NORLANDER L., MACCELLARO A.,			
RA	BAECKMAN A., BOELIN I., WOLF-WARTZ H.,			
RL	J. BACTERIOL. 173:1607-1616(1991).			
CC	-I- FUNCTION. INVOLVED IN CA(2+) REGULATION OF YOP EXPRESSION, WHICH			
CC	INCLUDES THE EXPORT PROCESS.			
CC	-I- SUBCELLULAR LOCATION: SECRETED.			
DR	EMBL; M57893; G155458; -.			
DR	PIR; B37314; B37314.			
KM	PLASMID; ANTIGEN; VIRULENCE.			
SO	SEQUENCE 326 AA; 37336 MW; 7D84E243 CRC32;			

Query Match Similarity	96.68%	Pred. NC 0.00e+00;	Length 326;
Best Local Similarity	96.68%	Mismatches 7;	Indels 0; Gaps 0
Matches 315;	Conservative		
Db	1	mlraeygnpqhflfedlekvrveqltghgsvleelvglvkdknidiskypkdxseffa	60
QY	196	MIRAEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKKNIDISKYPRDSEFFA	255
Db	61	nrvtddlellkklilayflpedaillkgshybnqjngfkrvkeflessprtgwelraffa	120
QY	256	NRVTDDLELLKKLILAYFLPEDTILKGGHYNDQNGIKRKEKELESSPNTQWELRPFMA	315
Db	121	vlhfgltadridddllkvlvdsmbhgydarekireelaetaelklysvlqaeinkhlss	180
QY	316	VMHFLGTADRIDDDDLTKIYVDSMNHGPARSKLREELAELEAKIYSVIOAEINKHLSS	375
Db	181	ggtlnhhksslnmdkolvygtideeifphasseykilekmppttqgegetekklyvsinfi	240
QY	376	SGTINHHKSSLNMDKNLIGYTDDEIFPHASSEYKILEKMPPTTQVDSSEKKIYSINDFL	435
Db	241	esekkrtgalgnlkdsysynkdnhelshfattedsksrplndlvsgkttqtsldstsrfs	300
QY	436	GSEKKRTGALGNLKNSSYSYNKDNNELSHFATTCSDKSRPLNDLVSGKTTQLSDITSRFS	495
Db	301	alealnrtfkgvdsymgrllldtsgk	326
QY	496	ALAEALNRTIQKVDYSWQRLDDTSGK	521
RESULT	3	STANDARD;	PRF; 170 AA.
ID	CAFLYERPE		
AC	P26948.		
DT	01-AUG-1992 (REL. 23, CREATED)		
DT	01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)		
DT	01-DEC-1992 (REL. 23, LAST ANNOTATION UPDATE)		

DE	F1 CAPSULE ANTIGEN PRECURSOR.
GN	CAP1.
OS	YERSINIA PESTIS.
OC	PLASMID PFR ^A .
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC	ENTEROBACTERIACEAE.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 91099503.
RA	GALYOV E.E., SMIRNOV O.Y., KARLISHEV A.V., VOLKOVOT K.I.,
RA	DENEZBUR A.I., NAZIMOV I.V., RUBTSOV K.S., ABRAMOV V.M.,
RA	DALVADYANZ S.M., ZAV'YALOV V.P.;
RL	FEBS LETT. 277:230-232(1990).
CC	I - SUBCELLULAR LOCATION: CAPSULE.
DR	EMBL; X61996; G48621; -.
DR	PIR; S13008; S13008.
KW	PLASMID; SIGNAL.
FT	SIGNAL. 21
FT	CHAIN 22 170
FT	DOMAIN 100 150
FT	POTENTIAL. F1 CAPSULE ANTIGEN.
FT	CONTAINS POTENTIAL ANTIGENIC DETERMINANTS
FT	THAT MAY STIMULATE T-CELLS.
SO	SEQUENCE 170 AA; 17666 MW; 354322B5 CRC32;

Query Match	31.0%;	Score 1100;	DB 2;	Length 170;
Best Local Similarity	100.0%;	Pred. No. 1.64e-160;		
Matches	170;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Db	1	mkksivaiailfgtiamanadi	tasttaactl	veparitly	kegapitl	indngidc	60
Oy	24	mkriissviala	lfgtia	anmad	tastta	atlv	83
Db	61	ellvgtllggyk	fgtts	svnf	daagdm	nyl	120
Oy	84	ellvgtllg	gkgt	stsvnf	daagdp	pyll	143
Db	121	pkvgeni	lv	gdav	lat	sgd	170
Oy	144	pkvneni	lv	gdav	lat	sgd	193

ID	RESULT	4	STANDARD	PRF.	168	AA.
AC	FM33	ECOLI				
DT	P15488;					
DT	01-APR-1990	(REL. 14, CREATED)				
DT	01-APR-1990	(REL. 14, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)				
DE	CS3	FIMBRIAL SUBUNIT A PRECURSOR (CS3 PILIN).				
OC	ESCHERICHIA COLI.					
OC	PROKARYOTA: GRACILICUTES, SCOTOBACTERIA; FACULTATIVELY ANAEROBIC ROD					
OC	ENTEROBACTERIACEAE.					
RN	[1]					
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.					
RC	STRAIN-PB176;					
RX	MEDLINE; 90158116.					
RA	JAJAJUKUARI M. B., THOMAS C. J., HALTER R., MANNING P. A.;					
RL	MOL. MICROBIOL. 3:1685-1695(1989).					
RN	[2]					
RN	SEQUENCE FROM N.A.					
RX	MEDLINE; 89032631.					
RA	BOYLAN M., SMYTH C. J., SCOTT J. R.;					
RL	INFECT. IMMUN. 56:3297-3300(1988).					
RN	[3]					
RP	SEQUENCE OF 23-45.					
RC	STRAIN-B9034A;					
RX	MEDLINE; 90036735.					
RA	HALL R. H., MANEVAL D. R. JR., COLLINS J. H., THEIBERT J. L.;					
RL	LEVINE M. M.;					
RA	J. BACTERIOL. 171:6372-6374(1989).					
CC	-1- FUNCTION: FIMBRINE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING					
CC	FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5					
CC	MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO					
CC	COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.					
CR	EMBL; J16944; G41161; -					

DR EMBL: M35657; G145627; -
 DR PIR: A34952; A34952.
 DR PIR: S07904; S07904.
 KW FIMBRIA; SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 168 CS3 FIMBRIAL SUBUNIT A.
 FT CONFLICT 83 83 N -> S (IN REF. 2).
 SQ SEQUENCE 168 AA; 17491 MW; 4D5CD89A CRC32.

Query Match 3.68; Score 127; DB 4; Length 168;
 Best Local Similarity 24.18; Pred. No. 3.28e-02;
 Matches 41; Conservative 47; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlklylllglsamsyslaaagplltkelalnvspaladepqnlstntg-v 59
 QY 24 MKRISSV-LAIALFGLTA-PANADLTASTATATLVEPARITLTYREGAPITMDNGT 81
 Db 60 -snltvgvltlntsltdtvsiaastnvsdtskngt-vtfahetnsaafatt-1stdnanl 116
 QY 82 DTELLVOTLTLGGYKCTTS-TSVNFTDAAGDPVYLTFTSODGNHOFITIKVIGKDSRDF 140
 Db 117 tld-magnativ-ktngsqplnplklttegnehlvsngyranltit 164
 QY 141 DISPKVNGENLVGDVVLATGSDFEVRSIGSKGK-LAAGKYTDVAVT 189

RESULT 5
 ID ACT3_YEAST STANDARD; PRT; 489 AA.

AC P80428;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE ACTIN-LIKE PROTEIN ACT3.
 GN ACT3 OR YJL081C OR J1012.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 94336725.
 RA HARATA M., KARMAN A., WINTERSBERGER U.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:8258-8262(1994).
 RN [2]
 RP ERRATUM.
 RA MEDLINE; 95024194.
 RA HARATA M., KARMAN A., WINTERSBERGER U.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:10757-10757(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE; 96093911.
 RA MIOSGA T., SCHAFF-GERSTENSCHLAGER I., CHALMATZIS N., BAUR A.,
 RA BOLES E., FOURNIER C., SCHMITT S., VELTEN C., WILHELM N.,
 RA ZIMMERMANN F.K.;
 RL YEAST 11:681-689(1995).
 CC -I- SIMILARITY: TO ACTIN. STRONG, TO OTHER ACTIN-LIKE PROTEINS
 CC -I- OF THE ARP4 SUBFAMILY.
 DR EMBL: X75317; G436808; -
 DR EMBL: X83502; G929875; -
 DR EMBL: Z49356; G1008244; -
 DR PIR: S47608; S47608.
 DR LISTA: SC01441; ACT3.
 DR SGD: L0000027; ACT3.
 DR PROSITE: PS01132; ACTINS_ACT_LINE.
 DR STRUCTURAL PROTEIN; CYTOSKELETON.
 KW SEQUENCE 489 AA; 54831 MW; C41435B1 CRC32.

Query Match 3.58; Score 123; DB 1; Length 489;
 Best Local Similarity 25.88; Pred. No. 9.09e-02;
 Matches 16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

Db 22 gsytlngysgdfpsilpsvygkytadgnkkifsegslprkdvklplle-ngly 80
 QY 93 GGKTKTSTSVNFTDAGDPVLTFTSODGNHOFITIKVIGKDSRDFDISPKVNGENLV 152

Db 81 fd 82
 QY 153 GD 154

RESULT 6
 ID MEDB_GITALA STANDARD; PRT; 857 AA.

AC 008014;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE MEDIAN BODY PROTEIN.
 OS GIARDIA LAMBLIA (GIARDIA INTESTINALIS).
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
 OC HEXAMITIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PORTLAND-1;
 RX MEDLINE; 93287123.
 RA MARSHALL J., HOLBERTON D.V.;
 RL J. MOL. BIOL. 231:521-530(1993).
 CC -I- FUNCTION: MAY HAVE A ROLE IN IMMOBILISING THE MICROTUBULES
 CC BETWEEN CELL DIVISIONS.
 CC -I- SUBCELLULAR LOCATION: MEDIAN BODY.
 CC -I- DOMAIN: SHOWS AN ALPHA-HELICAL COILED COIL STRUCTURE (30
 DR EMBL: X64517; G312671; -
 KW CYTOSKELETON; MICROTUBULES; COILED COIL; HEPTAD REPEAT PATTERN.
 SQ SEQUENCE 857 AA; 100583 MW; 5E2BBA84 CRC32;

Query Match 3.58; Score 124; DB 6; Length 857;
 Best Local Similarity 20.18; Pred. No. 7.06e-02;
 Matches 43; Conservative 71; Mismatches 82; Indels 18; Gaps 17;

Db 582 ervveeicqekennllkqptlelqgqratvretemallrekaneldgynreargen 641
 QY 205 QHTEED-LEKRVVEQLTGHOSSVLEELVOLVKRNIDISIKIDPRKDFEFA-NRYITD- 261
 Db 642 elmlldkalesdklrgdnvameel-telrekvqlleklyekardveemlelrhamd 700
 QY 262 DIELLK-KILAYF-LPEDITLKGGHYDNOQNGIKRV-K-EFLSSPNQ-WELRA-FWA 315
 Db 701 vdtlveekqrllemrlaelklkvnnyqjadakarleqgkldiefemind-nrrl 759
 QY 316 VMHFSLTADRIDDII-LKVIYDSMNHHGPARSKREBELAELTAEIKIVSVQAEINKHL 373
 Db 760 klqkv-elldktan-mek-lyeeykkldedqlkat 790
 QY 374 SSSGTTIHDKSINLMDKNLYG-YTD-ELEFKAS 405

RESULT 7
 ID PAS1_YARLI STANDARD; PRT; 2076 AA.

AC P34229;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE FATY ACID SYNTHASE, SUBUNIT BETA (EC 2.3.1.86) (CONTAINS: 3-
 DE HYDROXYPALMITOYL-[ACYL-CARRIER-PROTEIN] DEHYDRATASE (EC 4.2.1.61);
 DE ENOYL-[ACYL-CARRIER-PROTEIN] ACETYLTRANSFERASE (EC 1.3.1.19); [ACYL-
 DE CARRIER-PROTEIN] ACETYLTRANSFERASE (EC 2.3.1.38); [ACYL-CARRIER-
 DE PROTEIN] MALONYLTRANSFERASE (EC 2.3.1.39); AND S-ACYL FATY ACID
 DE SYNTHASE THIOESTERASE (EC 3.1.2.14)).
 GN PAS1.

OS YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CX 161-1 B ADEL A;
 RX MEDLINE; 91238709.
 RA KOETIG H., ROTTNER G., BECK K.-F., SCHWEIZER M., SCHWEIZER E.;
 RL MOL. GEN. GENET. 226:310-314(1991).

CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
CC THE BETA SUBUNIT CONTAINS DOMAINS FOR: [ACYL-CARRIER PROTEIN]
CC ACETYLTRANSFERASE AND MALONYLTRANSFERASE. S-ACYL FATTY ACID
CC SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND
CC 3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN] DEHYDRATASE.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+) .
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+) .
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + [ACYL-CARRIER PROTEIN] = COA
CC + ACETYL-[ACYL-CARRIER PROTEIN] .
CC -1- CATALYTIC ACTIVITY: MALONYL-COA + [ACYL-CARRIER PROTEIN] = COA
CC + MALONYL-[ACYL-CARRIER PROTEIN] .
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]
CC = 2-HEADCEHOYL-[ACYL-CARRIER PROTEIN] + H(2)O .
CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = 2,3-
CC DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH .
CC -1- CATALYTIC ACTIVITY: OLEOYL-[ACYL-CARRIER PROTEIN] + NAD(+) =
CC ACYL-CARRIER PROTEIN + OLEATE .
CC -1- SUBUNIT: FATTY ACID SYNTHETASE ARE [ALPHA(6)BETA(6)] HEXAMERS OF
CC TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA) .
CC EMBL: X59690; G297853; .
CC PIR: S15999; .
CC FATTY ACID BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME; OXIDOREDUCTASE;
CC TRANSFERASE; HYDROLASE; LIGASE; NAD; NADP .
CC DOMAIN 1 470 ACETYL TRANSFERASE .
CC DOMAIN 482 869 ENOYL REDUCTASE .
CC DOMAIN 1186 1647 DEHYDRATASE .
CC DOMAIN 1648 1869 MALONYL/PALMITOYL TRANSFERASE .
CC ACT_SITE 276 276 ACETYL TRANSFERASE (BY SIMILARITY) .
CC ACT_SITE 1832 1832 MALONYLTRANSFERASE (BY SIMILARITY) .
CC SEQUENCE 2076 AA; 230223 MW; E10A5234 CRC32; .

Query Match 3.5%; Score 123; DB 3; Length 2076;
Best Local Similarity 31.3%; Pred. No. 9, 09e-02;
Matches 25; Conservative 22; Mismatches 28; Indels 5; Gaps 5;

Db 1266 fdnrrrkefykylwfggsk-feldtdlt-eeliggddtlsgkaladtvhvgnbgeaf 1325
QY 119 TSQDGNHGHFTTKV-IGKSRDPDISPKNGENLVGDVLAATGSDPFVRSISKGKRL 177
DB 1326 v-gstsaqtv-fapmdfal 1343
QY 178 AAGKXTDAVTAVSNOEFMI 197

RESULT 8
AC P40555; STANDARD; PRT; 220 AA.
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HYPOTHELICAL 24.8 KD PROTEIN IN FPA3-BET1 INTERGENIC REGION.
GN Y110070.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
RA GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA RAUNDSEAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA WALSH S.V., WHITEHEAD S.;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z38113; G558397; .
DR EMBL: Z47047; G763339; .
DR PIR: S48450; S48450.
KW HYPOTHELICAL PROTEIN.
SQ SEQUENCE 220 AA; 24846 MW; B3911075 CRC32;

Query Match 3.4%; Score 120; DB 11; Length 220;
Best Local Similarity 22.8%; Pred. No. 1, 93e-01;
Matches 34; Conservative 39; Mismatches 69; Indels 7; Gaps 7;

Db 38 ktditqleay-fsvlegq-igmbsalvtpdy-prsdvdlqvtmrkvnmlkndln 94
QY 213 KVRVE-QLTGHSSVLEELVQLVKNDKIDISIKYPRRDSSEVFANRVITDIELKKILA 271
DB 95 hllqshvllnqfhnmvnsqndarrn-nddqaqyilpafissevpgpsdkaaklv 153
QY 272 YLEPDTILKGGHYNOJONGIKRVRKEFLSSPNTOWELR-AFNAVHPSLADRIDDDI 330
DB 154 ddkllstgnavhaanbsklqnlqmvvmkne 182
QY 331 LKVIYDSNMHHGDASKLRE-ELAEITLAE 358

RESULT 9
AC P25332; STANDARD; PRT; 333 AA.
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE PROBABLE RIBOKINASE (EC 2.7.1.15) .
GN RBK1 OR YCR36W OR YCR523 .
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RX MEDLINE: 91181345.
RA THERREY A., FAIRHEAD C., DUJON B.;
RL YEAST 6:521-534(1990).
CC -1- CATALYTIC ACTIVITY: ATP + D-RIBOSE = ADP + D-RIBOSE 5-PHOSPHATE.
CC -1- PATHWAY: FIRST STEP IN RIBOSE METABOLISM.
CC -1- SIMILARITY: BELONGS TO A FAMILY OF CARBOHYDRATE KINASES THAT
CC GROUPS TOGETHERS PERK, FRUK, GSK, IACC, RSK, AND SCRK .
CC EMBL: X56909; G4492; .
CC EMBL: X59720; E264378; .
CC PIR: S12918; KIBYRB.
CC LISTA: SC00940; RBK1.
CC SGD: I0001587; RBK1.
CC DR POSITE: PS00583; PERK_KINASES_1.
CC DR POSITE: PS00584; PERK_KINASES_2.
CC KW TRANSFERASE; KINASE.
CC SEQUENCE 333 AA; 36984 MW; 3E1772EC CRC32;

Query Match 3.4%; Score 120; DB 8; Length 333;
Best Local Similarity 23.2%; Pred. No. 1, 93e-01;
Matches 22; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

Db 235 klmmrkkgivmclgsgvlfcshepsvqfipaigvsvvdtgtagdtlglvltqly 294
QY 176 KLAAGKYDAVTAVTSNOEFMIRAYEQNPQHIEDLEKRVLEQULGHSSVLEELY-OLV 234
DB 295 gqetlsmalkfstlassltlqrgaaesmplykdv 329
QY 235 KDKNIDISIKIDPRKQSEVFANRVITDIELKKI 269

RESULT 10
AC P32497; STANDARD; PRT; 812 AA.
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE NUCLEAR TRANSPORT PROTEIN NIP1 .
GN NIP1 OR YMR309C OR YMR924.01C OR YMR952.11C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93066237.

[illegible]

SQ	SEQUENCE	558 AA;	62633 MW;	332AFEC3 CRC32;
Dd	Query Match	3.1%;	Score 110;	DB 8; Length 558;
OY	Best Local Similarity	22.4%;	Pred. No. 2.14e+00;	
OY	Matches	49; Conservative	61; Mismatches 91;	Indels 18; Gaps 15;
Dd	105 rskaflnstpsasqkqlaqelaglylhngggnasglilkndyqglvdrfaahpblvlkmre	164		
OY	295 RVKFFLSSPPTOMELRAFMN-VMHFS-LTRADR--DDDLKYIVDSMNHGDRSKLR	350		
Dd	165 dygtwknlgqvkvkfqqgvaeenarkqglgy-qvdeide-fnlrpnv-yleledqrlls	221		
OY	351 EL-A-EUTAEKLKIY--SVIQAELINKLLSSSGTINIHDKSINIMDKNLGYDTDEEIRKAS	405		
Dd	222 ss-eqlqigsgaalqt-lsendvnldslilyratqyidelaajdpqyaevqmndalig	219		
OY	406 AEVYLKMKPDQTIIQVGSEKKIYSINDFEGSENKRGAUGANKNSYS-Y-NKDNNELSH	463		
Dd	280 vqaetse-vgnlssnleagdpqlqlegatqsltg-lar	316		
OY	464 FATCSDKRPLNDLVSOIKTTQJSDITSRFNSATEALNR	502		
RESULT	15	STANDARD;	PRT;	710 AA.
ID	PTA_HAEIN			
AC	p45107;			
DT	01-NOV-1995 (REL. 32, CREATED)			
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	PHOSPHATE ACETYLTTRANSFERASE (EC 2.3.1.8) (PHOSPHOTRANSACETYLASE).			
GN	PTA OR H1203			
OS	HAEOPHIUS INFLUENZAE.			
OC	PROKARYOTA; GRACILICTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	PASTERELLACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-RD / KW20:			
RX	MEDLINE; 95350630.			
RA	FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,			
RA	KERLANAGE A.R., BUTL C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,			
RA	MCKENNEY K., STUTON G., FITZUGH W., FIELDS C.A., GOCCAYNE J.D.,			
RA	SCOTT J.D., SHIRLEY R., LIU L.-T., GLODER A., KELLEY J.M.,			
RA	WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,			
RA	WIEDERACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,			
RA	FINE L.D., FRITCHAM J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,			
RA	GHEHM C.L., MCCONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,			
RA	VENTER J.C.;			
RL	SCIENCE 269:496-512(1995).			
CC	-I- CATALYTIC ACTIVITY: ACETYL-COA + ORTHOPHOSPHATE - COA +			
CC	ACETYL-PHOSPHATE.			
CC	-I- SIMILARITY: IN THE N-TERMINAL HALF, TO COBYRIC ACID SYNTHASE.			
CC	-I- SIMILARITY: IN THE C-TERMINAL HALF, BELONGS TO THE PHOSPHATE			
CC	ACETYLTTRANSFERASE AND BUTYRYLTTRANSFERASE FAMILY.			
DR	EMBL; L45838; GI007082; .-			
DR	EMBL; U32799; G926270; .-			
KW	TRANSFERASE; ACYLTTRANSFERASE.			
SO	INIT_MET 0 BY SIMILARITY.			
SO	SEQUENCE 710 AA; 76385 MW; 6666EE6A CRC32;			
Query Match	3.1%;	Score 109;	DB 8; Length 710;	
Best Local Similarity	22.9%;	Pred. No. 2.70e+00;		
Matches	32; Conservative	45; Mismatches 54;	Indels 9; Gaps 8;	
Dd	79 gngsdvlllekivahnqgltknn-divvvvgllptkrkhgynsninyelagaldediyvaa	137		
OY	248 RKDSEVFNARKVIIDDILKKILAIFPEEDITLKGGH-IYNOLANGIKR-VK-EF-LESS	303		
Dd	138 patelepldkryeeaa-sifggknmpullgyvvvnknfnapvdsgutrltpalaeifdsfgh	196		
OY	304 PNTQM--ELRAFMAVMHFSLTRADRIDDIKLYIVDSNMHHGDARSKRRELAETLTKI	361		
Dd	197 nhsetevnr-flageaelki 215			

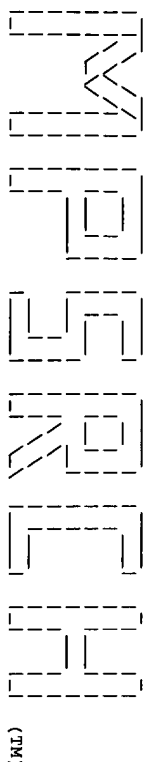
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Page 7

OY 362 YSVIOAEINKHLSSGTHNI 381

Search completed: Fri Apr 25 12:02:27 1997
job time : 52 secs.



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MPearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 18:31:48 1997; Maspar time 1301.65 Seconds
1337.742 Million cell updates/sec

Tabular output not generated.

Title: >US-08-699-716A-1
Description: (1-1566) from US08699716A.seq
Perfect Score: 1566
N.A. Sequence: 1 ATGGCCGATCATCATCATCA.....ATGACACGCTCTGTAATGA 1566
Comp: TACCCCGTAGTAGTACTACT.....TACTGTGACAGACCATTTACT

Scoring table: TABLE default
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

emb1-new11
1.BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VIR1 24:VIR2

Database:

genbank97
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:VRT4
53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7
74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13
80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
87:ROD7 88:ROD8 89:STR 90:SYN 91:DNA 92:VRT1 93:VRT2
94:VRT3 95:VRT4 96:VRT5 97:VRT6 98:VRT7 99:VRT8 100:VRT9
genbank-new11
101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
113:DNA 114:VRT
u-emb148_97
115:Part1 116:part2

Database:

Database:

Statistics: Mean 11.674; Variance 5.373; scale 2.173

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description Pred. No.
SUMMARIES

1	979	62.5	2100	33	YEPLCR	Yersinia pestis lcrG	0.00e+00
2	951	60.7	981	33	YEPLCR	Yersinia pseudotuberculosis	0.00e+00
3	947	60.5	2201	33	YEPLCR	Yersinia pseudotuberculosis	0.00e+00
4	903	57.7	975	33	YE108VANT	Y. enterocolitica V an	0.00e+00
5	901	57.5	975	33	YE108VANT	Y. enterocolitica V an	0.00e+00
6	899	57.4	975	33	YE527VANT	Y. enterocolitica V an	0.00e+00
7	897	57.3	975	33	YE808VANT	Y. enterocolitica V an	0.00e+00
8	767	49.0	1002	33	YE314VANT	Y. enterocolitica V an	0.00e+00
9	757	48.3	1002	33	YENCTVANT	Y. enterocolitica V an	0.00e+00
10	516	38.0	5383	33	YPCAF	Y. pestis genes catf,	0.00e+00
11	212	13.5	240	31	S75264	lcrGVH operon: lcrV-V	2.42e-154
12	53	3.4	521	80	HSU21500	WT1-W1ms' tumor supp	6.85e-19
13	31	2.0	670	74	HSU21500	Human chromosome 17q2	1.02e-03
14	31	2.0	670	74	RIC5IN12	Rice retroposon P-SIN	1.02e-03
15	31	2.0	1867	59	DDIPRKT	Dictyostelium discoid	1.02e-03
16	31	2.0	7407	76	HUMG1PRD	Human gene for gastr	1.02e-03
17	30	1.9	115	87	RNEDNRB7	Rattus norvegicus end	4.10e-03
18	30	1.9	205	44	P1MTRE	Polistes annularis (c	4.10e-03
19	29	1.9	271	82	MG1CMJ35	Mouse rearranged V(H)	1.61e-02
20	29	1.9	680	66	YSCFVN80	Yeast (S. cerevisiae)	1.61e-02
21	29	1.9	1800	63	SCPRTF	S. cerevisiae gene for	4.10e-03
22	30	1.9	1813	85	MUSIGHVJ2	Mouse Ig germ-line H-c	4.10e-03
23	29	1.9	1823	85	MUSIGHVY1	Mouse Ig germ-line H-c	4.10e-03
24	30	1.9	1839	63	SCU12825	Saccharomyces cerevis	1.61e-02
25	29	1.9	1888	57	ATHUBIOUF	Arabidopsis thaliana	1.61e-02
26	29	1.9	1920	43	OMMCYSB1	O. siroanet S-crysalis	1.61e-02
27	29	1.9	2359	49	CPMALPR	C. parvum gene for wal	1.61e-02
28	29	1.9	2363	64	PFARPHR	P. falciparum 240 kDa	1.61e-02
29	30	1.9	2836	54	SCYKL028W	S. cerevisiae chromoso	4.10e-03
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32	30	1.9	3178	40	S66865	pnt-painted (P) trans	4.10e-03
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38	30	1.9	12805	108	SC128XV	S. cerevisiae 12.8 Kbp	4.10e-03
39	30	1.9	25759	87	RNMHCG	Rat embryonic skeleta	4.10e-03
40	30	1.9	25759	87	RNMHCG	Rat embryonic skeleta	4.10e-03
41	30	1.9	28142	71	HS15886	Human DNA sequence fr	1.61e-02
42	29	1.9	31205	73	CEC06G1	Caenorhabditis elegans	4.10e-03
43	30	1.9	38461	73	HSU165H7	Human DNA sequence fr	4.10e-03
44	30	1.9	39960	110	HSU162C4	Human DNA sequence fr	4.10e-03
45	30	1.9	39960	73	HSU162C4	Human DNA sequence fr	4.10e-03

ALIGNMENTS

RESULT 1
LOCUS YEPLCR 2100 bp DNA BCT 27-MAR-1992
DEFINITION Yersinia pestis lcrG, lcrV, and lcrH genes, complete cds.
ACCESSION M26405
KEYWORDS 9155448
NID
SOURCE lcrG protein; lcrH protein; lcrV protein; V antigen.
ORGANISM 75kb virulence plasmid.
Yersinia pestis
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
1 (bases 1 to 2100)
Price,S.B., Leung,K.Y., Barve,S.S. and Straley,S.C.
Molecular analysis of lcrGVH, the V antigen operon of Yersinia
pestis
JOURNAL J. Bacteriol. 171, 5646-5653 (1989)
MEDLINE 90008806
COMMENT Computer readable copy of sequence [J. Bacteriol. (1989) In press]
Kindly submitted by Price,S.
07-AUG-1989.

FEATURES
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BASE COUNT	688 a	423 c	461 g								
ORIGIN		528 t									
Query Match	62.5%;	Score 979;	DB 33; Length 2100;								
Best Local Similarity	99.98;	Pred. No. 0.00e+00;									
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Qy	646 GTGGAACAACCT	TACTGFTCAT	GTGTTCTTCAG	TTTATAGAA	GAAATGTGTTCA	GTACTACAA	705				
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Qy	946 GTAAGCAT	TTTCTCTT	TAAACCG	CCGATCG	TATCGAT	GATGATAT	TTTGAAA	TGAT	TGTT	1005	
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OY	1186	TATAC	GATGAGAAGAAATTTTTTAAAGCCGCGCAGATGCAAAATCTTCGAGAAAATGCC	1245
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OY	1246	CAAAC	CACCATTCACAGTGGATGGAGCGACGAAAAAATAATAGTCTGATTAAGCACTTCTT	1305
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DEFINITION		Y.pseudotuberculosis V antigen gene.		
ACCESSION		X96802		
NID		g1405834		
KEYWORDS		V antigen.		
SOURCE		Yersinia pseudotuberculosis.		
ORGANISM		Yersinia pseudotuberculosis.		
REFERENCE		Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
AUTHORS		1 (bases 1 to 981)		
TITLE		Roggenkamp,A. and Heesemann,J.		
JOURNAL		Contribution of V antigen and anti-V antigen antibodies to an		
REFERENCE		infection with different Yersinia strains		
AUTHORS		Unpublished		
TITLE		2 (bases 1 to 981)		
JOURNAL		Roggenkamp,A.		
REFERENCE		Direct Submission		
AUTHORS		Submitted (22-MAR-1996) A. Roggenkamp, Hygiene und Microbiology,		
TITLE		University of Wuerzburg, Josef-Schneider Strasse 2, 97080		
JOURNAL		Wuerzburg, FRG		
FEATURES		Location/Qualifiers		
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RESULT 4
LOCUS YE96PVANT 975 bp DNA ECT 21-JUN-1996
DEFINITION Y. enterocolitica V antigen gene, strain Y-96-P.
ACCESSION X96801
NID 91405830
KEYWORDS V antigen.

SOURCE
ORGANISM
Yersinia enterocolitica (type 0:9).
Yersinia enterocolitica (type 0:9)
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE
1 (bases 1 to 975)
AUTHORS
Roggenkamp, A. and Heesemann, J.
TITLE
Contribution of V antigen and anti-V antigen antibodies to an
infection with different Yersinia strains
JOURNAL
Unpublished
2 (bases 1 to 975)
AUTHORS
Roggenkamp, A.
TITLE
Direct Submission
JOURNAL
Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG
FEATURES
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BASE COUNT 335 a 177 c 194 g 269 t
ORIGIN
Query Match 57.7%; Score 903; DB 33; Length 975;
Best Local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 936; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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QY 706 GATAAAATATATGATATTTCCATTAAATATGATCCAGAAAGATTCGAGGTTTTTGGC 765
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Db 301 gtaaaagagtlccttgaatcgcgcgaatcacacaatgagaaattgcgggcttcatggca 360
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RESULT 6
LOCUS YB527YANT 975 bp DNA BCT 21-JUN-1996
DEFINITION Y. enterocolitica V antigen gene, serotype 05/27.
ACCESSION X96800
NID g1405826
KEYWORDS V antigen.
SOURCE Yersinia enterocolitica.
ORGANISM Yersinia enterocolitica.
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 975)
AUTHORS Roggenkamp, A. and Heesemann, J.
TITLES Contribution of V antigen and anti-V antigen antibodies to an
infection with different Yersinia strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Roggenkamp, A.
TITLES Direct Submission
JOURNAL Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG
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BASE COUNT 339 a 173 c 192 g 271 t
ORIGIN
Query Match 57.4%; Score 899; DB 33; Length 975;
Best Local Similarity 96.4%; Pred. No. 0.00e+00;
Matches 934; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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Db 61 gtgggaacactactggtatgtgttcttcagtcttagaagaattggttcagttagccaa 120
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Db 121 gataaagaatagatattccatlaataatgatacccaaaagaattcggaagttttggc 180
Qy 706 GATTAATAATATGATATTTCATTAATATGATCCACAGAAAAGATTGCGAGTTTGGC 765
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Qy 1546 GATGACAGC 1554
RESULT 7
LOCUS YB808YANT 975 bp DNA BCT 21-JUN-1996
DEFINITION Y. enterocolitica V antigen gene, strain 8081.
ACCESSION X96798
NID g1405828
KEYWORDS V antigen.
SOURCE Yersinia enterocolitica (type 0:8).
ORGANISM Yersinia enterocolitica (type 0:8).
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 975)
AUTHORS Roggenkamp, A. and Heesemann, J.
TITLES Contribution of V antigen and anti-V antigen antibodies to an
infection with different Yersinia strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Roggenkamp, A.
TITLES Direct Submission
JOURNAL Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG
FEATURES
source Location/Qualifiers
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Qy 946	gtaatgatcttccttcaacgcgcgatcgatcgatgatgatcatatttgaagtgatgtt 1005
Db 421	gattcaatgatcatcatgatgtgatgaccccgtagcaagttcgctgaagaattagctgagct 480
Qy 1006	gattcaatgatcatcatgatgtgatgaccccgtagcaagttcgctgaagaattagctgagctt 1065
Db 481	accgcgcgaattaaagatttatctcagttatctcaagccgcgaattaaatgaatctgctagt 540
Qy 1066	accgcgcgaattaaagatttatctcagttatctcaagccgcgaattaaatgaatctgctagt 1125
Db 541	agtgaccacataatatacatatgaagaatcaatcaatcaatcgatgataaattatgatgt 600
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Qy 1246	caaacaccacataagagcgcagcgatgycagagagttgaggttatgctgctgggcgcaaaa 1280
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Qy 1281	-AATAGTCTCGATAAAGAGACTTTCTTGAGAGTGAAGATTAAGAACCGGGCGTTGGGT 1338
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Qy 1339	AATCTGAAAACTCATCTCTTAAATAAAGATTAAGATTAATCTCATCTTCCACAC 1398
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Qy 1399	ACCTGCTCGATTAAGTCCAGGCCGCTCAACGACTTGTTGTTAGCCAAAAAACACTGAGCTG 1458
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Qy 1459	TCTGATATTACATCAGCTTTTAATTACGATTAAGAACTGAACCTGATTCATTCAGAAA 1518
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Qy 1519	TATGATTCAGTGAACGCTGCTGTAAGATGACACG 1554
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DEFINITION	X enterocolitica V antigen gene, strain NCTC.
ACCESSION	X96797
KEYWORDS	g1405832
SOURCE	V antigen.
ORGANISM	Yersinia enterocolitica (type 0:8).
	Yersinia enterocolitica (type 0:8).
	Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.
REFERENCE	1 (bases 1 to 1002)
AUTHORS	Rogenkamp,A. and Heesemann,J.
TITLE	Contribution of V antigen and anti-V antigen antibodies to an infection with different Yersinia strains
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1002)
AUTHORS	Rogenkamp,A.
TITLE	Direct Submission
JOURNAL	Submitted (22-MAR-1996) A. Rogenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG
	Location/Qualifiers
	1...1002

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Oy	566	ATGATTAGAGCTTAGCGAACAACCCACAACATTTATTGAGGACTTGAAAAAGTTAGG	645			
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Oy	646	GTGGACAACACTTACTGTGTCATGTGTTCTTCAGTTTAGAAGAATTGGTTCAGTTACTCAA	705			
Db	121	gataaaaagatagatatlttcacattaaatatgatgccaaaaaagaattcggaggttttgc	180			
Oy	706	GATAAAATATAGATTAATTCATTAATATATGATCCACGAAGAAAGATTCCGAGGTTTTGCC	765			
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Oy	826	GAGGATGCCATTTCTTAAAGCGGTGCATTTATGACAACCAACTGCAAATATGGCATCAAGCA	885			
Db	301	gtaaaagaftctctggaatcatatcgccgaatacaaatggtgagttcggtgcgtcatgca	360			
Oy	886	GTAAGAAGTTCTTGTGATGATATCGCGCAATACACATGGGAATTCGGGCGTTTCATGGCA	945			
Db	361	gtaatgcaattctcttaaccgcgcgttcgatgcgatgatgatattttaagaatttgtt	420			
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Oy	1006	GATTCAATGAAATCATATGATGATGCGCGGATGCGAATTCGATGGAAGAATTACTGACCTT	1065			
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Oy	1246	CAAACACACATTT-----C-A-G-T-G---GA---TGG-G----AGC-----GA-CAAAAA	1280			
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Qy	1399	ACCTGCTCGAATGATCGAGCGCCTCACACACTTGCTGAGCCAAAACAACACTCAGCTG	1458
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Qy	1459	TCTGATTATCATCATCAGCTTTAATTCACTATTCAACACTGAACCGCTTCAATTCAGAAA	1518
Db	961	tatgattcagtaacacagctctctctatgatacagc	996
Qy	1519	TATGATTCACTGATGCAACGCTCTCTATAGATGACAG	1554
LOCUS	10	YPCAF	5383 bp
DEFINITION		Y. pestis genes cafI, cafIM, cafII, cafII and cafIR.	23-NOV-1995
ACCESSION		X61966	S90405 X57773
KEYWORDS		cafI gene; cafII gene; cafIM gene; cafIR gene; F1 antigen.	
SOURCE		Yersinia pestis.	
ORGANISM		Yersinia pestis.	
REFERENCE		Yersinia.	
AUTHORS		1 (bases 1 to 5383)	
TITLE		Galyov, E. E., Karlish, A. V., Chernovskaya, T. V., Dolgikh, D. A., Smirnov, O. Yu., Volkov, K. I., Abramov, V. M., and Zay'yalov, V. P.	
JOURNAL		Expression of the envelope antigen F1 of Yersinia pestis is mediated by the product of cafI gene having homology with the chaperone protein PapD of Escherichia coli	
REFERENCE		FEBS Lett. 286 (1-2), 79-82 (1991)	
AUTHORS		2 (bases 1 to 5383)	
TITLE		Galyov, E. E., Smirnov, O. Yu., Karlish, A. V., Volkov, K. I., Denesjuk, A. I., Nazimov, I. V., Rubtsov, K. S., Abramov, V. M., Dalvaadyanz, S. M., and Zay'yalov, V. P.	
JOURNAL		Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein. Putative T and B cell epitopes	
REFERENCE		FEBS Lett. 277 (1-2), 230-232 (1990)	
AUTHORS		3 (bases 1 to 5383)	
TITLE		Karlish, A. V.	
JOURNAL		Direct Submission	
REFERENCE		Submitted (24-JAN-1992) A. V. Karlish, Inst of Immunology, State Concern 'Biopreparation', 142380 Lyubchany, Moscow Region, USSR	
REMARK		4 (bases 1 to 5383)	
AUTHORS		Karlish, A. V., Galyov, E. E., Abramov, V. M., and Zay'yalov, V. P.	
TITLE		CafI gene and its role in the regulation of capsule formation of Y. pestis	
JOURNAL		FEBS Lett. 305 (1), 37-40 (1992)	
REFERENCE		5 (bases 1 to 5383)	
AUTHORS		Karlish, A. V., Galyov, E. E., Smirnov, O. Yu., Guzayev, A. P., Abramov, V. M., and Zay'yalov, V. P.	
TITLE		A new gene of the F1 operon of Y. pestis involved in the capsule biogenesis	
JOURNAL		FEBS Lett. 297 (1-2), 77-80 (1992)	
FEATURES		Location/Qualifiers	
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Qy	1399	ACCTGCTCGAATGATCGAGCGCCTCACACACTTGCTGAGCCAAAACAACACTCAGCTG	1458
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Qy	1459	TCTGATTATCATCATCAGCTTTAATTCACTATTCAACACTGAACCGCTTCAATTCAGAAA	1518
Db	961	tatgattcagtaacacagctctctctatgatacagc	996
Qy	1519	TATGATTCACTGATGCAACGCTCTCTATAGATGACAG	1554
LOCUS	10	YPCAF	5383 bp
DEFINITION		Y. pestis genes cafI, cafIM, cafII, cafII and cafIR.	23-NOV-1995
ACCESSION		X61966	S90405 X57773
KEYWORDS		cafI gene; cafII gene; cafIM gene; cafIR gene; F1 antigen.	
SOURCE		Yersinia pestis.	
ORGANISM		Yersinia pestis.	
REFERENCE		Yersinia.	
AUTHORS		1 (bases 1 to 5383)	
TITLE		Galyov, E. E., Karlish, A. V., Chernovskaya, T. V., Dolgikh, D. A., Smirnov, O. Yu., Volkov, K. I., Abramov, V. M., and Zay'yalov, V. P.	
JOURNAL		Expression of the envelope antigen F1 of Yersinia pestis is mediated by the product of cafI gene having homology with the chaperone protein PapD of Escherichia coli	
REFERENCE		FEBS Lett. 286 (1-2), 79-82 (1991)	
AUTHORS		2 (bases 1 to 5383)	
TITLE		Galyov, E. E., Smirnov, O. Yu., Karlish, A. V., Volkov, K. I., Denesjuk, A. I., Nazimov, I. V., Rubtsov, K. S., Abramov, V. M., Dalvaadyanz, S. M., and Zay'yalov, V. P.	
JOURNAL		Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein. Putative T and B cell epitopes	
REFERENCE		FEBS Lett. 277 (1-2), 230-232 (1990)	
AUTHORS		3 (bases 1 to 5383)	
TITLE		Karlish, A. V.	
JOURNAL		Direct Submission	
REFERENCE		Submitted (24-JAN-1992) A. V. Karlish, Inst of Immunology, State Concern 'Biopreparation', 142380 Lyubchany, Moscow Region, USSR	
REMARK		4 (bases 1 to 5383)	
AUTHORS		Karlish, A. V., Galyov, E. E., Abramov, V. M., and Zay'yalov, V. P.	
TITLE		CafI gene and its role in the regulation of capsule formation of Y. pestis	
JOURNAL		FEBS Lett. 305 (1), 37-40 (1992)	
REFERENCE		5 (bases 1 to 5383)	
AUTHORS		Karlish, A. V., Galyov, E. E., Smirnov, O. Yu., Guzayev, A. P., Abramov, V. M., and Zay'yalov, V. P.	
TITLE		A new gene of the F1 operon of Y. pestis involved in the capsule biogenesis	
JOURNAL		FEBS Lett. 297 (1-2), 77-80 (1992)	
FEATURES		Location/Qualifiers	
CDs		1..5383	
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QY 308 CATTAACTTACAGATGCGGGGATGCCATGACTTAACTTACTTCTCAGAGATG 367
DB 4916 gaataacacccaattcactacaaaagtattggcaagattcctagaattttgatatct 4975
QY 368 GAAATTAACCAATTCCTACAAAAGTATGCAAGATTCCTAGATTTGATATCT 427
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QY 428 CTCCTAAGTAAACGGGTGAACCTGTGGGGATGACGCGCTTGGCTACGGCAGCC 487
DB 5036 aggaattcttctgtcgtcctaattgtgtccaaagggttaacttcagcaggtataca 5095
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LOCUS S38727 240 bp DNA BCT 15-NOV-1992
DEFINITION lcrGVH operon: lcrV-v-antigen [Yersinia pseudotuberculosis, PY995,
Plasmid, 240 nt].
ACCESSION S38727
NID 9250552
KEYWORDS
SOURCE Yersinia pseudotuberculosis py995.
ORGANISM Yersinia pseudotuberculosis
REFERENCE
1 (bases 1 to 240)
Molin,V.L., Pokrovskaya,M.S., Telepnev,M.V., Kutyrev,V.V.,
Vidaeva,N.A., Filipov,A.A. and Smirnov,G.B.
The difference in the lcrV sequences between Y. pestis and Y.
pseudotuberculosis and its application for characterization of Y.
pseudotuberculosis strains
Microb. Pathog. 12 (3), 165-175 (1992)
JOURNAL
MEDLINE
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI g1bbseq 107284] from the original journal article.
This sequence comes from Fig. 2.
COMMENT
FEATURES
Location/Qualifiers
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BASE COUNT 96 a 39 c 48 g 57 t
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Best Local Similarity 94.28; Pred. No. 2,42e-154;
Matches 226; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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QY 1114 CATCTCTCTAGTAGTGACACCATTAATATCATGATTAATCCATTATCTCATGAGATAA 1173
DB 61 aattatattgattacagatgaagatttttaagccagtgacagatataatctc 120
QY 1174 AATTATATGCTATATACAGATGAAGATTTTAAAGCCGACGACAGATCAAAATTC 1233

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QY 1234 GAGAAATATCCCTCAAAACCAACCATTCAGGTGATGGAGACGAGAAAAATAGTCTCGATA 1293
DB 181 aagaattcttctgaagttgagaaaaaagaacccggggtgtgtgtaattcgaagactca 240
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LOCUS S75264 521 bp mRNA PRI 11-JUL-1995
DEFINITION WT1=Wilms' tumor suppressor protein [human, fetal kidney, mRNA, 521
nt].
ACCESSION S75264
NID 9896246
KEYWORDS
SOURCE human fetal kidney.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 521)
Hamilton,T.B., Barilla,K.C. and Romanuk,P.J.
High affinity binding sites for the Wilms' tumour suppressor
protein WT1
Nucleic Acids Res. 23 (2), 277-284 (1995)
JOURNAL
MEDLINE
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI g1bbseq 160293] from the original journal article.
This sequence comes from Fig. 1A.
COMMENT
FEATURES
Location/Qualifiers
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1..507
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Best Local Similarity 100.08; Pred. No. 6.85e-19;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 atggccatcatcatcatcatcatcatcatcatcaacagcagcgccatcgaa 53
QY 1 AUGGCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCA 53
RESULT 13
LOCUS HS021500 391 bp DNA PRI 08-JUN-1995
DEFINITION Human chromosome 17q21 clone ET10.
ACCESSION U21500
NID 9852476
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 391)
Verhebraat, Eutheria; Primates; Catarrhini; Homiidae; Homo.
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